

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:48:44 ; Search time 18 Seconds
(without alignments)
998.102 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDLDKSPVSLIFLM.....ITSEKDMHFSGLGCLLDLV 348

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
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5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|---------------------|-------------------|
| 1 | 1800 | 100.0 | 348 | 4 US-09-009-893A-6 | Sequence 6, Appl |
| 2 | 1800 | 100.0 | 348 | 4 US-09-489-155-6 | Sequence 6, Appl |
| 3 | 1635 | 90.8 | 480 | 3 US-08-795-088A-2 | Sequence 2, Appl |
| 4 | 1635 | 90.8 | 480 | 4 US-09-009-893A-2 | Sequence 2, Appl |
| 5 | 1635 | 90.8 | 480 | 4 US-09-489-155-2 | Sequence 2, Appl |
| 6 | 1579 | 87.7 | 480 | 4 US-09-069-023-34 | Sequence 34, Appl |
| 7 | 1554.5 | 86.4 | 445 | 3 US-08-859-167-2 | Sequence 2, Appl |
| 8 | 1554.5 | 86.4 | 445 | 3 US-09-109-273-2 | Sequence 2, Appl |
| 9 | 1554.5 | 86.4 | 445 | 3 US-09-276-993-2 | Sequence 2, Appl |
| 10 | 1554.5 | 86.4 | 445 | 4 US-09-723-450-2 | Sequence 2, Appl |
| 11 | 527 | 29.3 | 221 | 3 US-09-382-155-17 | Sequence 17, Appl |
| 12 | 527 | 29.3 | 221 | 3 US-09-074-044A-17 | Sequence 17, Appl |
| 13 | 383 | 21.3 | 84 | 3 US-09-074-044A-2 | Sequence 2, Appl |
| 14 | 369 | 20.5 | 84 | 3 US-09-382-155-2 | Sequence 2, Appl |
| 15 | 313 | 17.4 | 479 | 4 US-08-983-502-7 | Sequence 7, Appl |
| 16 | 313 | 17.4 | 479 | 4 US-08-516-747-7 | Sequence 7, Appl |
| 17 | 313 | 17.4 | 479 | 5 PCT-US96-10521-17 | Sequence 7, Appl |
| 18 | 311.5 | 17.3 | 478 | 4 US-09-009-893A-3 | Sequence 3, Appl |
| 19 | 311.5 | 17.3 | 478 | 4 US-09-489-155-3 | Sequence 3, Appl |
| 20 | 311 | 17.3 | 479 | 2 US-08-807-200-12 | Sequence 12, Appl |
| 21 | 311 | 17.3 | 479 | 2 US-09-382-155-28 | Sequence 28, Appl |
| 22 | 311 | 17.3 | 479 | 3 US-09-001-777-12 | Sequence 12, Appl |
| 23 | 311 | 17.3 | 479 | 3 US-09-074-044A-26 | Sequence 26, Appl |
| 24 | 311 | 17.3 | 479 | 3 US-09-074-044A-27 | Sequence 27, Appl |
| 25 | 311 | 17.3 | 479 | 3 US-09-074-044A-28 | Sequence 28, Appl |
| 26 | 309 | 17.2 | 479 | 3 US-08-852-782-3 | Sequence 3, Appl |
| 27 | 306 | 17.0 | 479 | 3 US-09-382-155-27 | Sequence 27, Appl |

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| 28 | 304.5 | 16.9 | 464 | 4 US-08-983-502-18 | Sequence 18, Appl |
| 29 | 304.5 | 16.9 | 464 | 4 US-09-516-747-18 | Sequence 18, Appl |
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| 31 | 303 | 16.8 | 479 | 3 US-09-382-155-26 | Sequence 26, Appl |
| 32 | 302.5 | 16.8 | 389 | 1 US-08-618-408B-4 | Sequence 4, Appl |
| 33 | 302.5 | 16.8 | 496 | 1 US-08-665-220-4 | Sequence 4, Appl |
| 34 | 302.5 | 16.8 | 496 | 3 US-09-291-692-4 | Sequence 2, Appl |
| 35 | 296.5 | 16.5 | 476 | 4 US-09-561-756-27 | Sequence 27, Appl |
| 36 | 296.5 | 16.5 | 476 | 4 US-09-227-721-37 | Sequence 27, Appl |
| 37 | 296.5 | 16.5 | 476 | 4 US-09-954-697-27 | Sequence 27, Appl |
| 38 | 261.5 | 14.5 | 335 | 4 US-08-983-502-16 | Sequence 16, Appl |
| 39 | 261.5 | 14.5 | 335 | 4 US-09-516-747-16 | Sequence 16, Appl |
| 40 | 261.5 | 14.5 | 335 | 5 PCT-US96-10521-16 | Sequence 16, Appl |
| 41 | 248.5 | 13.8 | 521 | 4 US-09-962-834A-2 | Sequence 2, Appl |
| 42 | 244 | 13.6 | 479 | 1 US-08-665-220-2 | Sequence 2, Appl |
| 43 | 244 | 13.6 | 479 | 3 US-09-291-692-2 | Sequence 2, Appl |
| 44 | 244 | 13.6 | 479 | 3 US-09-561-756-33 | Sequence 33, Appl |
| 45 | 244 | 13.6 | 479 | 4 US-09-227-721-33 | Sequence 33, Appl |

ALIGNMENTS

| | | | | | |
|---|-----|---|-----|--|--|
| RESULT 1 | | | | | |
| US-09-009-893A-6 | | | | | |
| Sequence 6, Application US/09009893A | | | | | |
| Patent No. 6623938 | | | | | |
| GENERAL INFORMATION | | | | | |
| APPLICANT: M. Chan | | | | | |
| APPLICANT: Rosen, Craig A. | | | | | |
| APPLICANT: Dixit, Vishva M. | | | | | |
| APPLICANT: Gentz, Reiner U. | | | | | |
| APPLICANT: Kenney, Joseph J. | | | | | |
| TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec | | | | | |
| FILE REFERENCE: 1488, 0970002 | | | | | |
| CURRENT APPLICATION NUMBER: US/09/009,893A | | | | | |
| CURRENT FILING DATE: 1998-02-21 | | | | | |
| PRIOR APPLICATION NUMBER: US 60/054,800 | | | | | |
| PRIOR FILING DATE: 1997-08-05 | | | | | |
| PRIOR APPLICATION NUMBER: US 60/034,205 | | | | | |
| PRIOR FILING DATE: 1997-01-21 | | | | | |
| NUMBER OF SEQ ID NOS: 35 | | | | | |
| SOFTWARE: PatentIn version 3.0 | | | | | |
| SEQ ID NO 6 | | | | | |
| LENGTH: 348 | | | | | |
| TYPE: PRT | | | | | |
| ORGANISM: Homo sapiens | | | | | |
| US-09-009-893A-6 | | | | | |
| Query Match | | | | | |
| Best Local Similarity 100.0%; Score 1800; DB 4; Length 348; | | | | | |
| Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | |
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| DB | 1 | MAEIGEDLDKSPVSLIFLMKDYMGKISKESFLDLVVELEKINLVAPDLDLLEKCL | 60 | | |
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| DB | 61 | KNHRIIDLKTIQKYQSVQAGTSYRNVLQAAIQSKLDPBNNRREPVKKSIOSENF | 120 | | |
| QY | 61 | KNHRIIDLKTIQKYQSVQAGTSYRNVLQAAIQSKLDPBNNRREPVKKSIOSENF | 120 | | |
| DB | 61 | KNHRIIDLKTIQKYQSVQAGTSYRNVLQAAIQSKLDPBNNRREPVKKSIOSENF | 120 | | |
| QY | 121 | LPOSIPERRYKMSKPLGICLLIDCIGNETELLRDFTSLGYEVOKFLHSMHGISOILG | 180 | | |
| DB | 121 | LPOSIPERRYKMSKPLGICLLIDCIGNETELLRDFTSLGYEVOKFLHSMHGISOILG | 180 | | |
| QY | 121 | LPOSIPERRYKMSKPLGICLLIDCIGNETELLRDFTSLGYEVOKFLHSMHGISOILG | 180 | | |
| DB | 121 | LPOSIPERRYKMSKPLGICLLIDCIGNETELLRDFTSLGYEVOKFLHSMHGISOILG | 180 | | |
| QY | 181 | QFACMPHRDYDSFVCLVSRGSGSVYGVDTGTHSGLPLHRIIRPFMGDSCYLAGKPKM | 240 | | |
| DB | 181 | QFACMPHRDYDSFVCLVSRGSGSVYGVDTGTHSGLPLHRIIRPFMGDSCYLAGKPKM | 240 | | |
| QY | 181 | QFACMPHRDYDSFVCLVSRGSGSVYGVDTGTHSGLPLHRIIRPFMGDSCYLAGKPKM | 240 | | |
| DB | 181 | QFACMPHRDYDSFVCLVSRGSGSVYGVDTGTHSGLPLHRIIRPFMGDSCYLAGKPKM | 240 | | |
| QY | 241 | FFIINYVYSGQLDESLLEVDGPAMKNTFFKQKRGKGLCTVAREADFFPSLCTADMSLLE | 300 | | |
| DB | 241 | FFIINYVYSGQLDESLLEVDGPAMKNTFFKQKRGKGLCTVAREADFFPSLCTADMSLLE | 300 | | |
| QY | 241 | FFIINYVYSGQLDESLLEVDGPAMKNTFFKQKRGKGLCTVAREADFFPSLCTADMSLLE | 300 | | |
| DB | 241 | FFIINYVYSGQLDESLLEVDGPAMKNTFFKQKRGKGLCTVAREADFFPSLCTADMSLLE | 300 | | |

Wed Sep 8 06:14:12 2004

us-10-713-208-6.open.ra1

Page 2

QY 301 QSHSPSLYLQCLSQKLRQERTIPGSGITSEKDMHFSGLCILLDVL 348
Db 301 QSHSPSLYLQCLSQKLRQERTIPGSGITSEKDMHFSGLCILLDVL 348

RESULT 2
US-09-489-155-6
Sequence 5, Application US/09489155
Patent No. 6680171
GENERAL INFORMATION
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Dixit, Vishva M.
APPLICANT: Gentz, Reiner L.
APPLICANT: Kenny, Joseph J.
TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Recep
FILE REFERENCE: 1488.0970002
CURRENT APPLICATION NUMBER: US/09/489,155
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/009,893
PRIOR FILING DATE: 1998-01-21
PRIOR APPLICATION NUMBER: US 60/034,205
PRIOR FILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapiens
US-09-489-155-6

Query Match 100.0%; Score 1800; DB 4; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.1e-183;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEIGEDLDKSDVSSILFLMKDYMGKISKEKSPFLDIYVELEKLNVAPODLLEKCL 60
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QY 61 KNHRIIDLTKTKIQKQKQSVQAGTSYRNVLQAAIQKSLKDPNNFEEBVKKSIOSEBAF 120
Db 61 KNHRIIDLTKTKIQKQKQSVQAGTSYRNVLQAAIQKSLKDPNNFEEBVKKSIOSEBAF 120
QY 121 LPOSIPEERYKMSKPIGICLLIDCIGNETELRLDFTSLGYEVQKFLHLSMHGISQILG 180
Db 121 LPOSIPEERYKMSKPIGICLLIDCIGNETELRLDFTSLGYEVQKFLHLSMHGISQILG 180
QY 181 QFACMPBHRDYSFVCLVSRGSSQSVYGVDTGHSGLPLHHIRRMFMGDSQCYLAGKXPM 240
Db 181 QFACMPBHRDYSFVCLVSRGSSQSVYGVDTGHSGLPLHHIRRMFMGDSQCYLAGKXPM 240
QY 241 FFIONVYVSDGQLEDSSILEVDGPANKNVEFKAQKRGCLCTVAREADFTMSLCTADMSILE 300
Db 241 FFIONVYVSDGQLEDSSILEVDGPANKNVEFKAQKRGCLCTVAREADFTMSLCTADMSILE 300
QY 301 QSHSPSLYLQCLSQKLRQERTIPGSGITSEKDMHFSGLCILLDVL 348
Db 301 QSHSPSLYLQCLSQKLRQERTIPGSGITSEKDMHFSGLCILLDVL 348

RESULT 3
US-08-795-088A-2
Sequence 2, Application US/08795088A
Patent No. 6242569
GENERAL INFORMATION
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Dixit, Vishva M.
APPLICANT: Gentz, Reiner L.
APPLICANT: Kenny, Joseph J.
TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor R
FILE REFERENCE: 1488.0970002
CURRENT APPLICATION NUMBER: US/09/009,893A

STREET: 75 Denise Drive
CITY: Hillsborough
STATE: California
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,088A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-001
TELEPHONE: (650) 343-4342
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-795-088A-2

Query Match 90.8%; Score 1635; DB 3; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.8e-166;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
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Db 157 KNHRIIDLTKTKIQKQKQSVQAGTSYRNVLQAAIQKSLKDPNNFEEBVKKSIOSEBAF 216
QY 107 ----EEBVKKSIOSEBAFIPGSIPEERYKMSKPIGICLLIDCIGNETELRLDFTSLGY 162
Db 217 LCAQGPVVKKSIOSEBAFIPGSIPEERYKMSKPIGICLLIDCIGNETELRLDFTSLGY 276
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Db 277 EVQKFLHLSMHGISQILGQFACMPBHRDYSFVCLVSRGSSQSVYGVDTGHSGLPLHHI 336
QY 223 RRMFMGDSQCYLAGKXPMFFIONVYVSDGQLEDSSILEVDGPANKNVEFKAQKRGCLCTVH 282
Db 337 RRMFMGDSQCYLAGKXPMFFIONVYVSDGQLEDSSILEVDGPANKNVEFKAQKRGCLCTVH 396
QY 283 READFTMSLCTADMSILEQSHSPSLYLQCLSQKLRQER 321
Db 397 READFTMSLCTADMSILEQSHSPSLYLQCLSQKLRQER 435

RESULT 4
US-09-009-893A-2
Sequence 2, Application US/09009893A
Patent No. 6623938
GENERAL INFORMATION
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Dixit, Vishva M.
APPLICANT: Gentz, Reiner L.
APPLICANT: Kenny, Joseph J.
TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor R
FILE REFERENCE: 1488.0970002
CURRENT APPLICATION NUMBER: US/09/009,893A

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/ CURRENT FILING DATE: 1998-02-21
/ PRIOR APPLICATION NUMBER: US 60/054,800
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: US 60/034,205
/ PRIOR FILING DATE: 1997-01-21
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: Patent version 3.0
/ SEQ ID NO 2
/ LENGTH: 480
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-009-893A-2

Query Match          90.8%; Score 1635; DB 4; Length 480;
Best Local Similarity 94.1%; Pred. No. 7,8e-16e;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

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QY 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLOAIOKSLKDPNSNFR----- 106
DB 157 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLOAIOKSLKDPNSNFR----- 216
QY 107 -----EPPVKKSIOSEAFLPQSIPEERYKMSKPLGICLIIDICGNTELLADPTFSLGY 162
DB 217 LGAQOEPPVKKSIOSEAFLPQSIPEERYKMSKPLGICLIIDICGNTELLADPTFSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLVSRGSGSVYGVQDTHSGLPJLHHI 222
DB 277 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLVSRGSGSVYGVQDTHSGLPJLHHI 336
QY 223 RRMFMGDSCPYLAGKPKMFFIQNYVVSQGLSDLSLEVDGPMKNVFRKQKGLCTVH 282
DB 337 RRMFMGDSCPYLAGKPKMFFIQNYVVSQGLSDLSLEVDGPMKNVFRKQKGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSPSLYLQCLSOXKLROER 321
DB 397 READPFWSLCTADMSLLEQSHSPSLYLQCLSOXKLROER 435

RESULT 5
US-09-489-155-2
/ Sequence 2, Application US/09489155
/ Patent No. 6680171
/ GENERAL INFORMATION:
/ APPLICANT: N1, Jlan
/ APPLICANT: Rosen, Craig A.
/ APPLICANT: Dixit, Vishva M.
/ APPLICANT: Gentz, Reiner L.
/ APPLICANT: Kenny, Joseph J.
/ TITLE OF INVENTION: I-FLICE A No. 6680171el Inhibitor of Tumor Necrosis Factor Recep
/ TITLE OF INVENTION: CD-95 Induced Apoptosis
/ FILE REFERENCE: 1488.0970002
/ CURRENT APPLICATION NUMBER: US/09/489,155
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US 09/009,893
/ PRIOR FILING DATE: 1998-01-21
/ PRIOR APPLICATION NUMBER: US 60/034,205
/ PRIOR FILING DATE: 1997-01-21
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: Patent version 3.0
/ SEQ ID NO 2
/ LENGTH: 480
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-489-155-2

Query Match          90.8%; Score 1635; DB 4; Length 480;
Best Local Similarity 94.1%; Pred. No. 7,8e-16e;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

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DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKSKSKESFLDVLVELEKLNVAAPDQDLLEKCL 156
QY 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLOAIOKSLKDPNSNFR----- 106
DB 157 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLOAIOKSLKDPNSNFR----- 216
QY 107 -----EPPVKKSIOSEAFLPQSIPEERYKMSKPLGICLIIDICGNTELLADPTFSLGY 162
DB 217 LGAQOEPPVKKSIOSEAFLPQSIPEERYKMSKPLGICLIIDICGNTELLADPTFSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLVSRGSGSVYGVQDTHSGLPJLHHI 222
DB 277 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLVSRGSGSVYGVQDTHSGLPJLHHI 336
QY 223 RRMFMGDSCPYLAGKPKMFFIQNYVVSQGLSDLSLEVDGPMKNVFRKQKGLCTVH 282
DB 337 RRMFMGDSCPYLAGKPKMFFIQNYVVSQGLSDLSLEVDGPMKNVFRKQKGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSPSLYLQCLSOXKLROER 321
DB 397 READPFWSLCTADMSLLEQSHSPSLYLQCLSOXKLROER 435

RESULT 6
US-09-069-023-34
/ Sequence 34, Appl:ication US/09069023A
/ Patent No. 6348573
/ GENERAL INFORMATION:
/ APPLICANT: Nunez, Gabriel
/ APPLICANT: Inohara, Naohiro
/ APPLICANT: Koseki, Takeyoshi
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
/ TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
/ FILE REFERENCE: UM-03333
/ CURRENT APPLICATION NUMBER: US/09/069,023A
/ CURRENT FILING DATE: 1998-04-27
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 34
/ LENGTH: 480
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-069-023-34

Query Match          87.7%; Score 1579; DB 4; Length 480;
Best Local Similarity 91.2%; Pred. No. 7,5e-16e;
Matches 309; Conservative 4; Mismatches 8; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKSKSKESFLDVLVELEKLNVAAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKSKSKESFLDVLVELEKLNVAAPDQDLLEKCL 156
QY 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLOAIOKSLKDPNSNFR----- 106
DB 157 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLOAIOKSLKDPNSNFR----- 216
QY 107 -----EPPVKKSIOSEAFLPQSIPEERYKMSKPLGICLIIDICGNTELLADPTFSLGY 162
DB 217 LGAQOEPPVKKSIOSEAFLPQSIPEERYKMSKPLGICLIIDICGNTELLADPTFSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLVSRGSGSVYGVQDTHSGLPJLHHI 222
DB 277 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLVSRGSGSVYGVQDTHSGLPJLHHI 336
QY 223 RRMFMGDSCPYLAGKPKMFFIQNYVVSQGLSDLSLEVDGPMKNVFRKQKGLCTVH 282
DB 337 RRMFMGDSCPYLAGKPKMFFIQNYVVSQGLSDLSLEVDGPMKNVFRKQKGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSPSLYLQCLSOXKLROER 321
DB 397 READPFWSLCTADMSLLEQSHSPSLYLQCLSOXKLROER 435

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RESULT 7
US-08-859-167-2
/ Sequence 2, Application US/08859167
/ Patent No. 6037461
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
/ TITLE OF INVENTION: USING THE SAME AND COMPOSITIONS FOR AND METHODS
/ TITLE OF INVENTION: OF MAKING THE SAME
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461, is
/ STREET: One Liberty Place, 46th floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: WINDOWS
/ SOFTWARE: Wordperfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/859,167
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Deluca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: TJU-
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 445 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-859-167-2

Query Match      86.4%; Score 1554.5; DB 3; Length 445;
Best Local Similarity 94.4%; Pred. No. 2.8e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

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QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKSFIDLIVLEKLNVAPODLLEKCL 60
 DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKSFIDLIVLEKLNVAPODLLEKCL 156
 QY 61 KNHRIIDLTKIÖKYKQSVÖGAGTSYRNVLÖAIÖKSLKDPNNFREBPVKKSIÖESEAF 120
 DB 157 KNHRIIDLTKIÖKYKQSVÖGAGTSYRNVLÖAIÖKSLKDPNNFR----- 202
 QY 121 LPOSIPERRYKMKSPGLGICLIIDICIGNETELRLDTFTSLGVEVÖKFLHLSMHGISOILG 180
 DB 203 --SIPERRYKMKSPGLGICLIIDICIGNETELRLDTFTSLGVEVÖKFLHLSMHGISOILG 259
 QY 181 QFACMPERHDYDSFVCVIVSRGSGSVYGVDTÖHSGPLPHIRRMFMGDSCPYLAGKPKM 240
 DB 260 QFACMPERHDYDSFVCVIVSRGSGSVYGVDTÖHSGPLPHIRRMFMGDSCPYLAGKPKM 319
 QY 241 FFIONYVSDGQLEDSLSLEVDPAMKNVFRKÖKRGCLCTVHREADFFWSICTADMSLLE 300
 DB 320 FFIONYVSEGGLEDSSLSLEVDPAMKNVFRKÖKRGCLCTVHREADFFWSICTADMSLLE 379
 QY 301 QSHSSPSLYLOCTLSÖKLRÖER 321
 DB 380 QSHSSPSLYLOCTLSÖKLRÖER 400

```

RESULT 8
US-09-109-273-2
/ Sequence 2, Application US/09109273
/ Patent No. 6063760
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
/ TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
/ TITLE OF INVENTION: OF MAKING THE SAME
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760, is
/ STREET: One Liberty Place, 46th floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: WINDOWS
/ SOFTWARE: Wordperfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/109,273
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/859,167
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Deluca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: TJU-
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 445 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-109-273-2

Query Match      86.4%; Score 1554.5; DB 3; Length 445;
Best Local Similarity 94.4%; Pred. No. 2.8e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

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QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKSFIDLIVLEKLNVAPODLLEKCL 60
 DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKSFIDLIVLEKLNVAPODLLEKCL 156
 QY 61 KNHRIIDLTKIÖKYKQSVÖGAGTSYRNVLÖAIÖKSLKDPNNFREBPVKKSIÖESEAF 120
 DB 157 KNHRIIDLTKIÖKYKQSVÖGAGTSYRNVLÖAIÖKSLKDPNNFR----- 202
 QY 121 LPOSIPERRYKMKSPGLGICLIIDICIGNETELRLDTFTSLGVEVÖKFLHLSMHGISOILG 180
 DB 203 --SIPERRYKMKSPGLGICLIIDICIGNETELRLDTFTSLGVEVÖKFLHLSMHGISOILG 259
 QY 181 QFACMPERHDYDSFVCVIVSRGSGSVYGVDTÖHSGPLPHIRRMFMGDSCPYLAGKPKM 240
 DB 260 QFACMPERHDYDSFVCVIVSRGSGSVYGVDTÖHSGPLPHIRRMFMGDSCPYLAGKPKM 319
 QY 241 FFIONYVSDGQLEDSLSLEVDPAMKNVFRKÖKRGCLCTVHREADFFWSICTADMSLLE 300
 DB 320 FFIONYVSEGGLEDSSLSLEVDPAMKNVFRKÖKRGCLCTVHREADFFWSICTADMSLLE 379
 QY 301 QSHSSPSLYLOCTLSÖKLRÖER 321
 DB 380 QSHSSPSLYLOCTLSÖKLRÖER 400

```
RESULT 9
US-09-276-993-2
; Sequence 2, Application US/09276993
; Patent No. 6207801
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801xis
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION NUMBER: US/09/276,993
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeJuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3438
; TELEFAX: (215) 568-3100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-276-993-2

Query Match      86.4%; Score 1554.5; DB 3; Length 445;
Best Local Similarity 94.4%; Pred. No. 2,8e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSILFLMKDYMGKISKESFLDLVLEKLNLAPODLLEKCL 60
DB 97 MAEIGEDLDKSDVSSILFLMKDYMGKISKESFLDLVLEKLNLAPODLLEKCL 156
QY 61 KNIRIDLTKIKQKYQSVGAGTSYRNVLQAAIQKSLKDPNNRREPVKKSIQESAF 120
DB 157 KNIRIDLTKIKQKYQSVGAGTSYRNVLQAAIQKSLKDPNNR----- 202
QY 121 LPSGIPBEERYKMKSPKLGICLIIDICGNETELLRDTFTSLGYEVQKFLHSMHGISQILG 180
DB 203 ---SIPBEERYKMKSPKLGICLIIDICGNETELLRDTFTSLGYEVQKFLHSMHGISQILG 259
QY 181 QFACMPBEHRDYSFVCVIVSRGSGSVYGVDPQTHSGLPFHIRRMFMGDSCEYLAKGPKM 240
DB 260 QFACMPBEHRDYSFVCVIVSRGSGSVYGVDPQTHSGLPFHIRRMFMGDSCEYLAKGPKM 319
QY 241 FFIQNYVSDGQLEDSSILLEVDPAMKNVEFKAQKRGCLCTVAREADPFWSLCTADMSLLE 300
DB 320 FFIQNYVSDGQLEDSSILLEVDPAMKNVEFKAQKRGCLCTVAREADPFWSLCTADMSLLE 379
QY 301 QSHSSPSLYLQCLSQKLRQER 321
DB 380 QSHSSPSLYLQCLSQKLRQER 400
```

```
RESULT 10
US-09-723-450-2
; Sequence 2, Application US/09723450
; Patent No. 6576751
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, An
; TITLE OF INVENTION: Compositions For And Methods Of Making The Same
; FILE REFERENCE: T012445
; CURRENT APPLICATION NUMBER: US/09/723,450
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6576751el Sequence
; US-09-723-450-2

Query Match      86.4%; Score 1554.5; DB 4; Length 445;
Best Local Similarity 94.4%; Pred. No. 2,8e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSILFLMKDYMGKISKESFLDLVLEKLNLAPODLLEKCL 60
DB 97 MAEIGEDLDKSDVSSILFLMKDYMGKISKESFLDLVLEKLNLAPODLLEKCL 156
QY 61 KNIRIDLTKIKQKYQSVGAGTSYRNVLQAAIQKSLKDPNNRREPVKKSIQESAF 120
DB 157 KNIRIDLTKIKQKYQSVGAGTSYRNVLQAAIQKSLKDPNNR----- 202
QY 121 LPSGIPBEERYKMKSPKLGICLIIDICGNETELLRDTFTSLGYEVQKFLHSMHGISQILG 180
DB 203 ---SIPBEERYKMKSPKLGICLIIDICGNETELLRDTFTSLGYEVQKFLHSMHGISQILG 259
QY 181 QFACMPBEHRDYSFVCVIVSRGSGSVYGVDPQTHSGLPFHIRRMFMGDSCEYLAKGPKM 240
DB 260 QFACMPBEHRDYSFVCVIVSRGSGSVYGVDPQTHSGLPFHIRRMFMGDSCEYLAKGPKM 319
QY 241 FFIQNYVSDGQLEDSSILLEVDPAMKNVEFKAQKRGCLCTVAREADPFWSLCTADMSLLE 300
DB 320 FFIQNYVSDGQLEDSSILLEVDPAMKNVEFKAQKRGCLCTVAREADPFWSLCTADMSLLE 379
QY 301 QSHSSPSLYLQCLSQKLRQER 321
DB 380 QSHSSPSLYLQCLSQKLRQER 400

RESULT 11
US-09-382-155-17
; Sequence 17, Application US/09382155B
; Patent No. 6160895
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
; TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; PRIOR FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
```

SEQ ID NO 17
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
US-09-382-155-17

Query Match 29.3%; Score 527; DB 3; Length 221;
Best Local Similarity 100.0%; Pred. No. 5.5e-48;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAAPDQDLLEKCL 156

QY 61 KNHRIIDLTKTIQKTKQKQSVQAGTSYRNVLQAAIQKSLKDPNNFR 106
DB 157 KNHRIIDLTKTIQKTKQKQSVQAGTSYRNVLQAAIQKSLKDPNNFR 202

RESULT 12

US-09-074-044A-17
Sequence 17, Application US/09074044A
Patent No. 6207458
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSES: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MISSOURI
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-074-044A-17

Query Match 29.3%; Score 527; DB 3; Length 221;
Best Local Similarity 100.0%; Pred. No. 5.5e-48;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAAPDQDLLEKCL 156

QY 61 KNHRIIDLTKTIQKTKQKQSVQAGTSYRNVLQAAIQKSLKDPNNFR 106

DB 157 KNHRIIDLTKTIQKTKQKQSVQAGTSYRNVLQAAIQKSLKDPNNFR 202

RESULT 13
US-09-074-044A-2

Sequence 2, Application US/09074044A
Patent No. 6207458
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSES: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MISSOURI
COUNTRY: USA
ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-074-044A-2

Query Match 21.3%; Score 383; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.8e-33;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAAPDQDLLEKCL 60
DB 8 MAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAAPDQDLLEKCL 67

QY 61 KNHRIIDLTKTIQKTKQ 77
DB 66 KNHRIIDLTKTIQKTKQ 84

RESULT 14

US-09-382-155-2
Sequence 2, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-08-24

EARLIER APPLICATION NUMBER: 08/074,044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 84
TYPE: PRT
ORGANISM: HUMAN HERPESVIRUS 8
US-09-382-155-2

Query Match 20.5%; Score 369; DB 3; Length 84;
Best Local Similarity 97.4%; Pred. No. 8,9e-32;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 MAIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDLYVEFEKLNVAPODLLEKCL 60
8 MAIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDLYVEFEKLNVAPODLLEKCL 67

Qy 61 KNIRIDLTKEIKQYKO 77
68 KNIRIDLTKEIKQYKO 84

RESULT 15
US-08-983-502-7
Sequence 7, Application US/08983502
Patent No. 6399327
GENERAL INFORMATION:
APPLICANT: David WALLACH
APPLICANT: Mark P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: Yuri V. GOLITSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=19
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-983-502-7

Query Match 17.4%; Score 313; DB 4; Length 479;
Best Local Similarity 26.8%; Pred. No. 1.4e-24;
Matches 95; Conservative 75; Mismatches 117; Indels 68; Gaps 14;

Qy 3 EIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDLYVEFEKLNVAPODLLEKCLXN 62
Db 107 QISEVSRSELKSFKFLQIEIISKCKLDDNMULDIFTEMKRYIIGSKLDIKRYCAQ 166

Qy 63 IIRIDLTKEIKQYKO-----SVQAGTSYRNVLOAIOKSLDPSNNFEPEPKSIQ 115
Db 167 INKSLKI-INDYEFSEKSRSSSLGSPDFSNGBELGVMTISDP---RE-----Q 215

Qy 116 BSEAFIPQSIPEERKRYKMSKPLIGLICITIDCIG-----NETEL-----LR 154
Db 216 DSES--QTL-DKVVQMKSKPGYCLINNENFAKAREKVEKLHSIRDRNGTHDAGALT 271

Qy 155 DFTSLGYEVCKFLHSMHGISOILGQFACMPERHDYDFVCVLVSRGSOVYGVQTH 214
Db 272 TTTEELHFEIKHDCQTYEQIYEILKIYQM-DHNMCCFICLISHDKGIIGTDQGE 330

Qy 215 SGLPLHHRFMWGSQPYLAGKPMFTIQ-----NY--VVSQGLDSSLLBYD--GP 264
Db 331 A-PIVELTSCFTGLKCPSLAGKPKVFFIOACQGDNYQGIPEVETDSSEQCYLENDLSP 388

Qy 265 AMKNVEFFKAQKRGKGLCTVHREADFWSLCTADWSLLEQSHSPSLYLOCLSGKLRQ 319
Db 389 QTRVTP-----DEADFLIGMAIVNVCVYRNPAEGTWIQLCSLSRE 431

Search completed: September 8, 2004, 05:52:28
Job time : 62 secs

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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:48:38 / Search time 58 Seconds
(without alignments)
1695.285 Million cell updates/sec

Title: US-10-713-208-6

Perfect score: 1800

Sequence: 1 MATIGEDLDKSDVSLIFLM.....ITRSDMHFSSVLTLLDVL 348

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1800 | 100.0 | 348 | 2 | AAW69230 I-FLICE-2 |
| 2 | 1800 | 100.0 | 348 | 7 | ADAI0619 Human inh |
| 3 | 1774 | 98.6 | 366 | 2 | AAW05788 Human MAC |
| 4 | 1774 | 98.6 | 462 | 3 | AAW67419 Usurpin-b |
| 5 | 1635 | 90.8 | 384 | 2 | AAW05791 WRIT alpb |
| 6 | 1635 | 90.8 | 480 | 2 | AAW58578 Human FIN |
| 7 | 1635 | 90.8 | 480 | 2 | AAW69715 Human Cas |
| 8 | 1635 | 90.8 | 480 | 2 | AAW69229 I-FLICE-1 |
| 9 | 1635 | 90.8 | 480 | 2 | AAW76631 Human CFL |
| 10 | 1635 | 90.8 | 480 | 2 | AAW05787 Human MAC |
| 11 | 1635 | 90.8 | 480 | 2 | AAW57454 Human FLI |
| 12 | 1635 | 90.8 | 480 | 3 | AAW57606 Human apo |
| 13 | 1635 | 90.8 | 480 | 3 | AAW67418 Usurpin-a |
| 14 | 1635 | 90.8 | 480 | 3 | AAW03960 FLICE-1lk |
| 15 | 1635 | 90.8 | 480 | 5 | ABW09294 Human FLI |
| 16 | 1635 | 90.8 | 480 | 7 | ADAI0615 Human inh |
| 17 | 1635 | 90.8 | 491 | 3 | AAW03964 FLIP with |
| 18 | 1630 | 90.6 | 391 | 4 | AAW09601 Human gen |
| 19 | 1630 | 90.6 | 391 | 4 | AAW01591 Novel hum |
| 20 | 1630 | 90.6 | 391 | 5 | ABW78973 Human apo |
| 21 | 1630 | 90.6 | 391 | 7 | ADCA6232 Human neo |
| 22 | 1630 | 90.6 | 391 | 7 | AAW39801 Human gen |
| 23 | 1630 | 90.6 | 480 | 2 | AAW78903 Human GI |
| 24 | 1618 | 89.9 | 479 | 2 | AAW76625 Human FLI |
| 25 | 1579 | 87.7 | 480 | 3 | AAW59414 Human CIA |

| | | | | | |
|----|--------|------|-----|---|--------------------|
| 26 | 1554.5 | 86.4 | 445 | 2 | AAW90107 Human FLA |
| 27 | 1554.5 | 86.4 | 445 | 2 | AAW26086 Human FLA |
| 28 | 1228 | 68.3 | 302 | 2 | AAW05792 MRIT-ND1 |
| 29 | 1128 | 62.7 | 264 | 2 | AAW05790 Human ant |
| 30 | 1018 | 56.6 | 481 | 2 | AAW76632 Mouse CFL |
| 31 | 1018 | 56.6 | 481 | 3 | AAW03958 FLICE-1lk |
| 32 | 1018 | 56.6 | 481 | 5 | ABW09295 Mouse FLI |
| 33 | 1018 | 56.6 | 483 | 2 | AAW76626 Mouse FLI |
| 34 | 1006.5 | 55.9 | 484 | 5 | ABW09292 Mouse FLI |
| 35 | 1006.5 | 55.9 | 484 | 6 | ABW9383 Amino aci |
| 36 | 978 | 54.3 | 230 | 2 | AAW05793 MRIT-Bam |
| 37 | 711.5 | 39.5 | 291 | 3 | AAW67420 Usurpin-9 |
| 38 | 683 | 37.9 | 175 | 2 | AAW05794 MRIT-D/S |
| 39 | 661.5 | 36.8 | 270 | 5 | AAW26110 Human FLA |
| 40 | 540 | 30.0 | 227 | 2 | AAW05795 MRIT beta |
| 41 | 527 | 29.3 | 221 | 2 | AAW78904 Human GI |
| 42 | 527 | 29.3 | 221 | 2 | AAW76630 Human CFL |
| 43 | 527 | 29.3 | 221 | 2 | AAW05789 Human MAC |
| 44 | 527 | 29.3 | 221 | 2 | AAW57455 Human FLI |
| 45 | 527 | 29.3 | 221 | 3 | AAW03959 FLICE-1lk |

ALIGNMENTS

RESULT 1
AAW69230 standard; protein; 348 AA.
ID
XX
AC AAW69230;
XX
DT 18-FEB-1999 (first entry)
XX
DE I-FLICE-2 protein.
XX
KW I-FLICE-2; PADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease;
KW CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis;
KW CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease;
KW multiple sclerosis; head injury; cancer; autoimmune disorder; therapy;
KW viral infection; graft versus host disease; graft rejection.
XX
OS Homo sapiens.
XX
PN WO9831801-AI.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US000969.
XX
PR 21-JAN-1997; 97US-003420SP.
PR 05-AUG-1997; 97US-005460OP.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
XX
PI Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
XX WPI: 1998-414100/35.
XX N-PSDB; AAW44807.
XX
DR New inhibitory polypeptides of FLICE - used to develop products for
XX treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis, cancers,
XX autoimmune disorders, viral infection or graft rejection.
XX
PS Claim 9; Fig 4; 118pp; English.
XX
CC This sequence is an inhibitor of of Fas-ligand associated with death
XX domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-2. The
XX proteins can inhibit both TNFR-1 and CD-95 induced apoptosis. These are
XX the first examples of a naturally occurring catalytically inactive
XX caspase that can act as a dominant negative inhibitor of apoptosis. The
XX polypeptides and agonists can be used for treating e.g. Alzheimer's
XX disease, Parkinson's disease, rheumatoid arthritis, septic shock, sepsis,

CC stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
 CC cell death associated with cardiovascular disease, polycystic kidney
 CC disease, apoptosis of endothelial cells in cardiovascular disease,
 CC degenerative liver disease, multiple sclerosis (MS) and head injury
 CC damage. Antagonists of the polypeptides can be used for treating cancers
 CC (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-
 CC dependent tumours, and cancers of the breast, ovary, prostate, bone,
 CC liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic
 CC lupus erythematosus, immune-related glomerulonephritis, rheumatoid
 CC arthritis), and viral infections (e.g. herpes viruses, pox viruses and
 CC adenoviruses), graft versus host disease, acute disease, acute graft
 CC rejection, and chronic graft rejection. The products can also be used for
 CC detection, diagnosis and drug screening

XX Sequence 348 AA;
 SQ

Query Match 100.0%; Score 1800; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 5,6e-172;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYGKGIKSKSFLLVVELEKLNVAAPDQDLLEKCL 60
 DB 1 MAEIGEDLDKSDVSSLIPLMKDYGKGIKSKSFLLVVELEKLNVAAPDQDLLEKCL 60
 QY 61 KNIHRIDLKTKIQKQKQSVQAGTSYRNVLQAAIQKSLDPSNNFREBPVKKSIOSEAF 120
 DB 61 KNIHRIDLKTKIQKQKQSVQAGTSYRNVLQAAIQKSLDPSNNFREBPVKKSIOSEAF 120
 QY 121 LPOSIPERRYKMKSKPLGICLIIDCIGNETELLADFTPSIGYEVQKFLHSMHGISOILG 180
 DB 121 LPOSIPERRYKMKSKPLGICLIIDCIGNETELLADFTPSIGYEVQKFLHSMHGISOILG 180
 QY 181 QFACMPERHDYDSFVFCVLVSRGSSQSVYGVDTGSLPLHTRRMFMGDSCEYLAKKPKM 240
 DB 181 QFACMPERHDYDSFVFCVLVSRGSSQSVYGVDTGSLPLHTRRMFMGDSCEYLAKKPKM 240
 QY 241 FFIONYVVSQGLEBSSLLLEVDPAMKNVEFKAQKRGCLCTVAREADFFWMSLCTADMSLE 300
 DB 241 FFIONYVVSQGLEBSSLLLEVDPAMKNVEFKAQKRGCLCTVAREADFFWMSLCTADMSLE 300
 QY 301 QSHSSPSLYLQCLSQKLRQERGTIPGSGITSEKMDHMFSSLGICILLDVL 348
 DB 301 QSHSSPSLYLQCLSQKLRQERGTIPGSGITSEKMDHMFSSLGICILLDVL 348

RESULT 2
 ADA10619
 ID ADA10619 standard; protein, 348 AA.
 AC ADA10619;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human inhibitor of FLICE (I-FLICE-2) protein.
 XX
 OS Human, I-FLICE-2; inhibitor of FLICE; FADD-like ICE;
 XX tumour necrosis factor receptor-1 inhibitor; TNFR-1 inhibitor;
 XX CD-95 induced apoptosis; apoptosis associated disease;
 XX Alzheimer's disease; rheumatoid arthritis; stroke; osteoporosis;
 XX ischaemia; septic shock; degenerative liver disease;
 XX cardiovascular disorder; aberrant cell survival; neurologic;
 XX anti-rheumatic; vasotropic; hepatotropic; osteopathic; cardiac;
 XX cerebroprotective; antibacterial; antiarthritis; vasodilator.
 XX
 OS Homo sapiens.
 XX
 XX US2003087339-A1.
 XX
 PD 06-MAY-2003.
 XX
 XX 21-JAN-1998; 98US-00009893.
 XX
 XX 21-JAN-1997; 97US-0034205P.
 XX
 PR 21-JAN-1997; 97US-0034205P.

PR 05-AUG-1997; 97US-0054800P.
 XX
 XX (NIJ/J) NI J.
 XX (ROSE/) ROSEN C A.
 XX (DIXI/) DIXIT V M.
 XX (GENT/) GENTZ R L.
 XX (KENN/) KENNY J J.
 XX
 XX NI J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
 XX WPI, 2003-576674/54.
 XX N-PSDB; ADA10618.
 DR
 PT New I-FLICE-1 (inhibitor of FLICE 1) or I-FLICE-2 nucleic acids, useful
 PT for treating diseases associated with apoptosis e.g., Alzheimer's
 PT disease, rheumatoid arthritis, stroke, osteoporosis, ischemia or septic
 PT shock.
 XX
 XX Claim 1; Fig 4A-4C; 48pp; English.
 XX
 XX The present invention relates to the isolation of novel human I-FLICE-1
 CC (inhibitor of FLICE (FADD-like ICE)) and I-FLICE-2 proteins, and the
 CC polynucleotide sequences encoding them. The I-FLICE-1 and I-FLICE-2
 CC proteins are novel inhibitors of tumour necrosis factor receptor-1 (TNFR-
 CC 1) and CD-95 induced apoptosis. Also disclosed are vectors, host cells
 CC and recombinant methods for producing the I-FLICE proteins. The sequences
 CC e.g. Alzheimer's disease, rheumatoid arthritis, stroke, osteoporosis,
 CC ischaemia, septic shock, degenerative liver disease, and cardiovascular
 CC disorders. They are also useful for diagnosing diseases or disorders
 CC associated with aberrant cell survival in an individual. The present
 CC sequence represents human I-FLICE-2.
 XX
 SQ Sequence 348 AA;
 Query Match 100.0%; Score 1800; DB 7; Length 348;
 Best Local Similarity 100.0%; Pred. No. 5,6e-172;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYGKGIKSKSFLLVVELEKLNVAAPDQDLLEKCL 60
 DB 1 MAEIGEDLDKSDVSSLIPLMKDYGKGIKSKSFLLVVELEKLNVAAPDQDLLEKCL 60
 QY 61 KNIHRIDLKTKIQKQKQSVQAGTSYRNVLQAAIQKSLDPSNNFREBPVKKSIOSEAF 120
 DB 61 KNIHRIDLKTKIQKQKQSVQAGTSYRNVLQAAIQKSLDPSNNFREBPVKKSIOSEAF 120
 QY 121 LPOSIPERRYKMKSKPLGICLIIDCIGNETELLADFTPSIGYEVQKFLHSMHGISOILG 180
 DB 121 LPOSIPERRYKMKSKPLGICLIIDCIGNETELLADFTPSIGYEVQKFLHSMHGISOILG 180
 QY 181 QFACMPERHDYDSFVFCVLVSRGSSQSVYGVDTGSLPLHTRRMFMGDSCEYLAKKPKM 240
 DB 181 QFACMPERHDYDSFVFCVLVSRGSSQSVYGVDTGSLPLHTRRMFMGDSCEYLAKKPKM 240
 QY 241 FFIONYVVSQGLEBSSLLLEVDPAMKNVEFKAQKRGCLCTVAREADFFWMSLCTADMSLE 300
 DB 241 FFIONYVVSQGLEBSSLLLEVDPAMKNVEFKAQKRGCLCTVAREADFFWMSLCTADMSLE 300
 QY 301 QSHSSPSLYLQCLSQKLRQERGTIPGSGITSEKMDHMFSSLGICILLDVL 348
 DB 301 QSHSSPSLYLQCLSQKLRQERGTIPGSGITSEKMDHMFSSLGICILLDVL 348

RESULT 3
 AA05788
 ID AA05788 standard; protein, 366 AA.
 AC AA05788;
 XX
 XX 02-AUG-1999 (first entry)
 XX
 XX Human MACH related inducer of toxicity MCHT alpha 2.
 XX
 DE

XX MRIT alpha 2; MACH related inducer of toxicity; human; apoptosis;
 KW anti-apoptotic; cancer; autoimmune disease; angiogenesis;
 KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
 KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
 KW aplastic anaemia; myocardial infarction; therapy.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 XX Active-site 262..266
 XX
 PN MO9918230-A2.
 XX
 PD 15-APR-1999.
 XX
 PF 07-OCT-1998; 98MO-US021132.
 XX
 PR 07-OCT-1997; 97US-00946226.
 XX
 PA (UNIM) UNIV WASHINGTON.
 XX
 PI Chaudhary PM;
 XX
 DR WPI: 1999-277275/23.
 DR N-PSDB; AAX25509.
 XX
 PT Identifying regulators of MACH-related inducer of toxicity.
 XX
 PS Claim 14; Fig 1G; 78pp; English.
 XX
 CC The present sequence represents novel human MACH-related inducer of
 CC toxicity (MRIT) isoform MRIT alpha 2, a CED-4 homologue. Multiple
 CC isoforms of MRIT have been identified, some of which function to induce
 CC caspase dependent apoptosis in mammalian cells, e.g. MRIT alpha 1 (see
 CC AAY05787) and MRIT beta 1 (see AAY05789), while others have anti-
 CC apoptotic activity, e.g. MRIT alpha 2. Selective enhancers and inhibitors
 CC of MRIT apoptotic activity can be identified and used to treat diseases
 CC mediated by the dysfunction of programmed cell death or proliferation. A
 CC cell accumulation disorder such as cancer, autoimmune disease, viral
 CC infection, angiogenesis or atherosclerosis is treated by administering an
 CC agent that selectively enhances MRIT apoptotic activity, thereby inducing
 CC apoptosis in a subject. A disorder of cell loss, such as a
 CC neurodegenerative disorder, including Alzheimer's disease, Parkinson's
 CC disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial
 CC infarction or AIDS can be treated by administering an agent that
 CC selectively inhibits MRIT apoptotic activity
 XX
 XX Sequence 366 AA;
 SQ
 Query Match 98.6%; Score 1774; DB 2; Length 366;
 Best Local Similarity 94.5%; Pred. No. 2,5e-169;
 Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
 QY 1 MAEIGEDLDKSDVSSILFLMKDYGSGKISKESKFLDLVLEKLNLYAPDQDLLEKCL 60
 DB 1 MAEIGEDLDKSDVSSILFLMKDYGSGKISKESKFLDLVLEKLNLYAPDQDLLEKCL 60
 QY 61 KNHHRIDLTAKIKYKQSVGAGTSRVNLYQAAIQKSLKDPNNR----- 106
 DB 61 KNHHRIDLTAKIKYKQSVGAGTSRVNLYQAAIQKSLKDPNNR----- 106
 QY 107 -----EEPVKKSIOSESAFLPOSIPERVKYKSKPLGICILIDCIGNETELLADTFTSLGY 162
 DB 121 LGAQGEVVKKSIOSESAFLPOSIPERVKYKSKPLGICILIDCIGNETELLADTFTSLGY 180
 QY 163 EVQGFELHLSHGSIQLIGFACMPERHDVDFYCVIVSSGSGSQSYGVQDQTHSGPLHHI 222
 DB 181 EVQGFELHLSHGSIQLIGFACMPERHDVDFYCVIVSSGSGSQSYGVQDQTHSGPLHHI 240
 QY 223 RRMFMGSCCYLAGKPMFPIQYVYVSDQLEDSSILEVDGPMKQVEPKAKQGLCTVH 282
 DB 241 RRMFMGSCCYLAGKPMFPIQYVYVSDQLEDSSILEVDGPMKQVEPKAKQGLCTVH 300

QY 283 READFFWLSCTADMSLEQSHSSPSLYLQCLSQKLRQERGTIPSGITESKDMHPSISLGC 342
 DB 301 READFFWLSCTADMSLEQSHSSPSLYLQCLSQKLRQERGTIPSGITESKDMHPSISLGC 360
 QY 343 ILDDVL 348
 DB 361 ILDDVL 366
 RESULT 4
 ID AAY67419 standard; protein; 462 AA.
 XX
 AC AAY67419;
 XX
 DT 12-MAY-2000 (first entry)
 XX
 DE Usurpin-beta polypeptide.
 XX
 KW Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;
 KW usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
 KW caspase; cyostatic; antiParkinsonian; antidiabetic.
 XX
 OS Homo sapiens.
 XX
 PN MO200003023-A1.
 XX
 PD 20-JAN-2000.
 XX
 PF 07-JUL-1999; 99MO-CA000615.
 XX
 PR 08-JUL-1998; 98US-0092005P.
 XX
 PA (MERI) MERCK FROSTT CANADA INC.
 XX
 PI Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;
 XX
 DR WPI: 2000-160929/14.
 DR N-PSDB; AAZ56988.
 XX
 PT Novel recombinant DNA molecules and polypeptides for treating apoptosis
 PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
 PT disease.
 XX
 PS Claim 6; Fig 10B; 69pp; English.
 XX
 CC The invention provides recombinant nucleic acid molecules encoding
 CC usurpin-alpha (lacking the first death effector domain (DED) or its
 CC prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are
 CC useful for in vitro and in vivo identification of usurpin-procaspase-8
 CC interaction inhibitor. Usurpin is useful as modulator of the sensitivity
 CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
 CC is useful for treating diseases like autoimmune diabetes, cancer and
 CC Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8
 CC interaction are also useful for treating various diseases mediated by
 CC apoptosis. Usurpin provides an attractive model for modulating caspase
 CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be
 CC regulated at several levels in the presence of usurpin, conferring
 CC resistance to Fas-ligand cell death. The present sequence represents the
 CC usurpin-beta polypeptide
 XX
 SQ Sequence 462 AA;
 Query Match 98.6%; Score 1774; DB 3; Length 462;
 Best Local Similarity 94.5%; Pred. No. 3,5e-169;
 Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
 QY 1 MAEIGEDLDKSDVSSILFLMKDYGSGKISKESKFLDLVLEKLNLYAPDQDLLEKCL 60
 DB 97 MAEIGEDLDKSDVSSILFLMKDYGSGKISKESKFLDLVLEKLNLYAPDQDLLEKCL 156
 QY 61 KNHHRIDLTAKIKYKQSVGAGTSRVNLYQAAIQKSLKDPNNR----- 106

| | | | |
|----|-----|--|-----|
| Db | 157 | KNHRIIDAKTKIQKTKYQAGCTSYRNVLOALQKSLKDSNNFRHLNGRSKEXORLKEQ | 216 |
| QY | 107 | ---EBPVKKSIOESEAFIPQSIPEBRYKMSKPIGLCIIIDCIGNETELLIDTFTSLGY | 162 |
| Db | 217 | IGAQQBPVKKSIQSESEAFIPQSIPEBRYKMSKPIGLCIIIDCIGNETELLIDTFTSLGY | 276 |
| QY | 163 | EVCKFHLTMHGISOILGOFACMPHRDVSVCVLVRGSSQSVYGVDOHSLPLHHI | 222 |
| Db | 277 | EVCKFHLTMHGISOILGOFACMPHRDVSVCVLVRGSSQSVYGVDOHSLPLHHI | 336 |
| QY | 223 | RRFMGDSCPYLAGKEMFPIQNYVVSQGLDESSLLEVDSPAMKNVEFKAKRGGLTVH | 282 |
| Db | 337 | RRFMGDSCPYLAGKEMFPIQNYVVSQGLDESSLLEVDSPAMKNVEFKAKRGGLTVH | 396 |
| QY | 283 | REKDFPWSICTADMSLLEQSHSPSLYLQCLSQKLRORGTIPGSGITESHKDMHFPSSLGC | 342 |
| Db | 397 | REKDFPWSICTADMSLLEQSHSPSLYLQCLSQKLRORGTIPGSGITESHKDMHFPSSLGC | 456 |
| QY | 343 | ILLDVL348 | |
| Db | 457 | ILLDVL462 | |

| | |
|----------|-------------------------------------|
| RESULTS | |
| AAV05791 | |
| ID | AAV05791 standard; protein: 384 AA. |
| XX | |
| AC | AAV05791; |
| XX | |
| DT | 02-AUG-1999 (first entry) |

MRIT alpha 3 polypeptide.
 MRIT alpha 3; MACH related inducer of toxicity; human; apoptosis;
 anti-apoptotic; cancer; autoimmune disease; angiodenesis;
 atherosclerosis; neurodegenerative disease; Alzheimer's disease;
 Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
 aplastic anaemia; myocardial infarction; therapy; mutant.
 Homo sapiens.
 Synthetic.
 W09918230-A2.
 15-APR-1999.
 07-OCT-1998; 98WO-US021132.
 07-OCT-1997; 97US-00946226.
 (UNIW) UNIV WASHINGTON.
 Chaudhary PM;
 WPI; 1999-277275/23.
 Identifying regulators of MACH-related inducer of toxicity.
 Example 2; Page; 78pp; English.
 The present sequence represents MRIT alpha 3, comprising amino acid
 residues 97-480 of novel human MACH-related inducer of toxicity MRIT
 alpha 1 (see AAY05787). This deletion mutant was used to examine the
 interaction of MRIT alpha 1 with caspases. The results indicated that
 PLIC-p20 binding to MRIT alpha 1 does not require the N-terminal 96
 amino acids. The invention provides multiple isoforms of MRIT (see
 AAY05787-89), isolated active fragments of which have either pro-
 apoptotic or anti-apoptotic activity. Selective enhancers and inhibitors
 of MRIT apoptotic activity can be identified and used to treat diseases
 mediated by the dysfunction of programmed cell death or proliferation,
 such as cancer or a neurodegenerative disorder. Note: the present
 sequence is not shown in the specification but is derived from the MRIT

| | | |
|---------------------------|-------------------------------------|--|
| CC | alpha 1 sequence given in figure 1F | |
| XX | | |
| SQ | Sequence 384 AA; | |
| | Score 1635; DB 2; Length 384; | |
| Query Match | 90.8%; | |
| Best Local Similarity | 94.1%; | |
| Matches 319; Conservative | 2; Mismatches 0; | |
| | Indels 18; Gaps 1; | |

```

QY      1 MAEIEDDDKSDVSSLLFLMKDDYMGSKISKEKSFJDLVVELKXNLVAPQDLLEKCL 60
Db      1 MAEIEDDDKSDVSSLLFLMKDDYMGSKISKEKSFJDLVVELKXNLVAPQDLLEKCL 60
QY      61 KNHHTIDKTKIQYKYSVQAGTSYRNLQALQCSLKDPSNNR----- 106
Db      61 KNHHTIDKTKIQYKYSVQAGTSYRNLQALQCSLKDPSNNRNLHNGSKSKEQLKEQ 120
QY      107 ----EEPVKKSIOSEAFPLQSIPEERYKSKSPGLICLIIDCIGNETELLRDFTFSIGY 162
Db      121 IGAQGEPEPKKSIOSEAFPLQSIPEERYKSKSPGLICLIIDCIGNETELLRDFTFSIGY 180
QY      163 EVQKXELHLSMGISQIIIGQFACMPBEHRDDSPFCVLVSHSGSSQSYGVGDQTHSGLPPLHI 222
Db      181 EVQKXELHLSMGISQIIIGQFACMPBEHRDDSPFCVLVSHSGSSQSYGVGDQTHSGLPPLHI 240
QY      223 REMFNGDSCPYLACKPMAPFTIQNVVSDGLEDDSSLLEVDPAMKNVEFPAKQKGLCTVH 282
Db      241 REMFNGDSCPYLACKPMAPFTIQNVVSEGLEDDSSLLEVDPAMKNVEFPAKQKGLCTVH 300
QY      283 READPFMSICTADMSLLEQSHSPSYLYCQLSQKLRQER 321
Db      301 READPFMSICTADMSLLEQSHSPSYLYCQLSQKLRQER 339

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| | |
|----|---|
| | RESULT 6 |
| ID | AAM58578 |
| ID | AAM58578 standard; protein; 480 AA. |
| AC | AAM58578; |
| DT | 07-SEP-1996 (first entry) |
| XX | |
| DE | Human FIN-1. |
| KW | Human; FIN-1; FLICE inhibitor-1; ICE-IAP7; death effector domain; DED; |
| KM | apoptosis-related protein; caspase; viral infection; cancer; tumour; |
| KW | diagnosis; ischaemic injury; neuro-degenerative disorder. |
| OS | Homo sapiens. |
| XX | |
| PN | EP841399-A2. |
| PD | 13-MAY-1996. |
| PF | 10-NOV-1997; 97PE-00309003. |
| PR | 12-NOV-1996; 96US-00748086. |
| XX | |
| PA | (SMIT) SMITHKLINE BEECHAM CORP. |
| PI | Rikly K. Emery JG; |
| DR | MP1; 1998-252943/23. |
| DR | N-PSSB; AAV31175. |
| PT | New nucleic acid encoding human apoptosis-related protein - used for diagnosis and treatment of e.g. viral infections, tumour, ischaemic injury and neuro-degenerative disorders. |
| XX | |
| PS | Claim 11; Page 25-27; 48pp; English. |
| CC | The present sequence represents human FIN-1 (FLICE inhibitor-1), which is a caspase. FLICE (ICE-IAP7) is a protease of the interleukin-converting enzyme family; a protein involved in the regulation of cell death. A host |

cell, comprising a vector containing FIN-1 encoding DNA, can be used to produce FIN-1. The vector containing the DNA can be used for producing a cell which expresses a polypeptide by transforming or transfecting the cell with it so that the cell expresses the polypeptide encoded the human cDNA contained in the vector. The polypeptide or its antagonist can be used in the treatment of patients needing FIN-1 by in-vivo administration. Conditions which may be treated include viral infection, tumours (especially solid tumours), ischaemic injury (e.g. stroke or myocardial infarction), neurodegenerative disorders (e.g. Alzheimer's or Parkinson's disease), osteoporosis, osteoarthritis, poly cystic kidney disease, chronic degenerative liver disease, acquired immunodeficiency syndrome (AIDS) and aplastic anaemia. The polynucleotides may also be used for chromosome identification

XX Sequence 480 AA:

Query Match 90.8%; Score 1635; DB 2; Length 480;
Best Local Similarity 94.1%; Pred. No. 3,6e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVLEKLNVAAPQDLLEKCL 60
97 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVLEKLNVAAPQDLLEKCL 156
61 KNHRIDLKTKIKYKQSVGAGTSYRNVLQALIKSLKDPENNFR----- 106
157 KNHRIDLKTKIKYKQSVGAGTSYRNVLQALIKSLKDPENNFR----- 216
107 ----EEPVKKSIOESSEAFIPQSIPEERYMKSKEPLGICIIDICIGNETELRLDTFTSLGY 162
217 LGAQGEVVKKSIOESSEAFIPQSIPEERYMKSKEPLGICIIDICIGNETELRLDTFTSLGY 276
163 EVQKFLHLSMHGISOILGQFACMPHEHDYDSFVCVLVSRGSGSYVGVDTHTSGPLNHI 222
277 EVQKFLHLSMHGISOILGQFACMPHEHDYDSFVCVLVSRGSGSYVGVDTHTSGPLNHI 336
223 RRFMGDSCEPYLAGKPKMFPIQNYVVSDDQLEDSLSLEVDGPAMKNVFFKAKRGCLCTVH 282
337 RRFMGDSCEPYLAGKPKMFPIQNYVVSDDQLEDSLSLEVDGPAMKNVFFKAKRGCLCTVH 396
283 READPFMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
397 READPFMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 7

AAW69715 standard; protein; 480 AA.

XX AAW69715;

XX 24-NOV-1998 (first entry)

XX Human Casper protein.

XX Casper; caspase-eight-related protein; human; apoptosis.

XX Homo sapiens.

XX WO9833883-A1.

XX 06-AUG-1998.

XX 05-FEB-1998; 98WO-US002117.

XX 05-FEB-1997; 97US-00795088.

XX (TULIA-) TULARIK INC.

XX Shu H, Goeddel DV;

XX WPI; 1998-437440/37.

XX N-PSDB; AAW50436.

XX New Casper protein involved in regulation of apoptosis - used, e.g. to identify specific modulators, identify or isolate similar sequences and PT in gene therapy.

XX Claim 1; Page 22-23; 29pp; English.

XX This is the amino acid sequence of a novel human protein, designated CC Casper (for caspase-eight-related protein), that is involved in CC regulation of apoptosis. The sequence is deduced from an isolated cDNA CC clone (see AAW50436). Casper protein interacts with FADD and is recruited CC to Fas. It also interacts with caspase-8 and caspase-3, and with TRAF1 CC and TRAF2. A claimed isolated polypeptide comprises the full-length CC Casper amino acid sequence, or a fragment of at least 6 consecutive amino CC acid residues including at least one of residues 1-96, 1-202, 1-435, 78- CC 480, 192-480, 390-480 or residue 360. The isolated protein, or cells that CC express the protein, can be used to screen for agents, e.g. antibodies or CC T-cell receptors, that specifically modify the binding of Casper to a CC target, and thus its function

XX Sequence 480 AA:

Query Match 90.8%; Score 1635; DB 2; Length 480;
Best Local Similarity 94.1%; Pred. No. 3,6e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVLEKLNVAAPQDLLEKCL 60
97 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVLEKLNVAAPQDLLEKCL 156
61 KNHRIDLKTKIKYKQSVGAGTSYRNVLQALIKSLKDPENNFR----- 106
157 KNHRIDLKTKIKYKQSVGAGTSYRNVLQALIKSLKDPENNFR----- 216
107 ----EEPVKKSIOESSEAFIPQSIPEERYMKSKEPLGICIIDICIGNETELRLDTFTSLGY 162
217 LGAQGEVVKKSIOESSEAFIPQSIPEERYMKSKEPLGICIIDICIGNETELRLDTFTSLGY 276
163 EVQKFLHLSMHGISOILGQFACMPHEHDYDSFVCVLVSRGSGSYVGVDTHTSGPLNHI 222
277 EVQKFLHLSMHGISOILGQFACMPHEHDYDSFVCVLVSRGSGSYVGVDTHTSGPLNHI 336
223 RRFMGDSCEPYLAGKPKMFPIQNYVVSDDQLEDSLSLEVDGPAMKNVFFKAKRGCLCTVH 282
337 RRFMGDSCEPYLAGKPKMFPIQNYVVSDDQLEDSLSLEVDGPAMKNVFFKAKRGCLCTVH 396
283 READPFMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
397 READPFMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 8

AAW69229 standard; protein; 480 AA.

XX AAW69229;

XX 16-OCT-1998 (first entry)

XX I-FLICE-1 protein.

XX I-FLICE-1; FADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease;

XX CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis;

XX CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease;

XX multiple sclerosis; head injury; cancer; autoimmune disorder; therapy;

XX viral infection; graft versus host disease; graft rejection.

XX Homo sapiens.

XX WO9831801-A1.

XX 23-JUL-1998.

PF 21-JAN-1998; 98MO-US000969.
 XX
 PR 21-JAN-1997; 97US-0034205P.
 PR 05-AUG-1997; 97US-0054800P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
 PI WPI; 1998-414100/35.
 DR N-PSDB; AAV44806.
 XX
 PT New inhibitory polypeptides of FLICE - used to develop products for
 PT treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis, cancers,
 PT autoimmune disorders, viral infection or graft rejection.
 XX
 PS Claim 9; Fig 1; 118pp; English.

CC This sequence is an inhibitor of of Fas-ligand associated with death
 CC domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-1. The
 CC proteins can inhibit both TNF-1 and CD-95 induced apoptosis. These are
 CC the first examples of a naturally occurring catalytically inactive
 CC caspase that can act as a dominant negative inhibitor of apoptosis. The
 CC polypeptides and agonists can be used for treating e.g. Alzheimer's
 CC disease, Parkinson's disease, rheumatoid arthritis, septic shock, sepsis,
 CC stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
 CC cell death associated with cardiovascular disease, polycystic kidney
 CC disease, apoptosis of endothelial cells in cardiovascular disease,
 CC degenerative liver disease, multiple sclerosis (MS) and head injury
 CC damage. Antagonists of the polypeptides can be used for treating cancers
 CC (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-
 CC dependent tumors, and cancers of the breast, ovary, prostate, bone,
 CC liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic
 CC lupus erythematosus, immune-related glomerulonephritis, rheumatoid
 CC arthritis), and viral infections (e.g. herpes viruses, pox viruses and
 CC adenoviruses), graft versus host disease, acute disease, acute graft
 CC rejection, and chronic graft rejection. The products can also be used for
 CC detection, diagnosis and drug screening
 CC
 XX

Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3.6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSLIFLMKDYMGKISKSEKFLDVLVELEKLNVAAPQDLLEKCL 60
 DB 97 MAEIGEDLDKSDVSLIFLMKDYMGKISKSEKFLDVLVELEKLNVAAPQDLLEKCL 156
 QY 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
 DB 157 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
 QY 107 ----EEPVKKSIOSESAFLPQSIPEERYMKSKPLGICLIIDICIGNETELRLDTFTSLGY 162
 DB 217 LGAQGEFVKKSIQSESAFLPQSIPEERYMKSKPLGICLIIDICIGNETELRLDTFTSLGY 276
 QY 163 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLYSRGSGQSYGVDTHTSGPLPHI 222
 DB 277 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLYSRGSGQSYGVDTHTSGPLPHI 336
 QY 223 RRMFMGDSCTYLAGKPKMFFIQNYVSDQLDSSLLLEVDPAMKNVFEFAQKRGCLTVH 282
 DB 337 RRMFMGDSCTYLAGKPKMFFIQNYVSDQLDSSLLLEVDPAMKNVFEFAQKRGCLTVH 396
 QY 283 READFFWSLCTADMSLLEQSHSSPSLIYLOCLSQKLRQER 321
 DB 397 READFFWSLCTADMSLLEQSHSSPSLIYLOCLSQKLRQER 435

RESULT 9
 AAV76631

ID AAV76631 standard; protein; 480 AA.

AC AAV76631;

DT 12-JUL-1999 (first entry)

DE Human CFLIP-L protein.

KM Death effector domain; human; murine; anti-apoptotic; treatment;

KM HIV infection; autoimmune disease; FLIP protein.

OS Homo sapiens.

XX DE19713393-A1.

PD 08-OCT-1998.

PF 01-APR-1997; 97DE-01013393.

PR 01-APR-1997; 97DE-01013393.

XX (TSCN/) TSCNPP J.

PI Tschopp J, Thome M, Burns K, Imler M, Hahne M, Schroeder M;

PI Schneider P, Bodmer J, Steiner V, Rimoldi D, Hoffmann K, French EL;

DR WPI; 1998-532710/46.

DR N-PSDB; AAV61937.

PT New DNA encoding for anti-apoptotic gene product - used to treat HIV

PT infections and autoimmune diseases.

XX Claim 20; Fig 4B; 45pp; German.

CC This invention describes novel human and mouse anti-apoptotic gene
 CC products which contain at least one death effector domain. The products
 CC of the invention are used in the treatment of HIV infections and
 CC autoimmune diseases
 CC
 XX

Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3.6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSLIFLMKDYMGKISKSEKFLDVLVELEKLNVAAPQDLLEKCL 60
 DB 97 MAEIGEDLDKSDVSLIFLMKDYMGKISKSEKFLDVLVELEKLNVAAPQDLLEKCL 156
 QY 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
 DB 157 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
 QY 107 ----EEPVKKSIOSESAFLPQSIPEERYMKSKPLGICLIIDICIGNETELRLDTFTSLGY 162
 DB 217 LGAQGEFVKKSIQSESAFLPQSIPEERYMKSKPLGICLIIDICIGNETELRLDTFTSLGY 276
 QY 163 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLYSRGSGQSYGVDTHTSGPLPHI 222
 DB 277 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLYSRGSGQSYGVDTHTSGPLPHI 336
 QY 223 RRMFMGDSCTYLAGKPKMFFIQNYVSDQLDSSLLLEVDPAMKNVFEFAQKRGCLTVH 282
 DB 337 RRMFMGDSCTYLAGKPKMFFIQNYVSDQLDSSLLLEVDPAMKNVFEFAQKRGCLTVH 396
 QY 283 READFFWSLCTADMSLLEQSHSSPSLIYLOCLSQKLRQER 321
 DB 397 READFFWSLCTADMSLLEQSHSSPSLIYLOCLSQKLRQER 435

RESULT 10
 AA05787
 ID AA05787 standard; protein; 480 AA.

XX AC AAY05787;
 XX 02-AUG-1999 (first entry)
 XX
 XX Human MACH related inducer of toxicity Mrit alpha 1.
 DE
 XX Mrit alpha 1; MACH related inducer of toxicity; human; apoptosis;
 KW pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
 KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
 KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
 KW aplastic anaemia; myocardial infarction; therapy.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Region 1..165 /note="death effector domain homology region"
 FT Region 140..178 /note="Bcl-2 homology region"
 FT Region 196..228 /note="Bcl-2 homology region"
 FT Region 258..289 /note="Bcl-2 homology region"
 FT Region 299..350 /note="Bcl-2 homology region"
 FT Region 301..480 /note="Bcl-2 homology region"
 FT Region /note="caspase homology region"
 FT Region 356..397 /note="Bcl-2 homology region"
 FT Active-site 358..362
 XX
 XX W09918230-A2.
 XX
 XX 15-APR-1999.
 PD
 PF 07-OCT-1998; 98WO-US021132.
 XX
 PR 07-OCT-1997; 97US-00946226.
 XX
 PA (UNIV) UNIV WASHINGTON.
 XX
 PI Chaudhary PM;
 XX
 XX WPI; 1999-277275/23.
 DR N-PSDB; AAX25508.
 XX
 XX Identifying regulators of MACH-related inducer of toxicity.
 PT
 XX Example 1; Fig 1F; 78pp; English.
 PS
 XX The present sequence represents novel human MACH-related inducer of
 CC toxicity (Mrit) isoform Mrit alpha 1, a CED-4 homologue that interacts
 CC simultaneously with caspases and Bcl-2 family polypeptides, and which has
 CC pro-apoptotic activity. Multiple isoforms of Mrit have been identified,
 CC some of which function to induce caspase dependent apoptosis in mammalian
 CC cells; e.g. Mrit alpha 1 and Mrit beta 1 (see AAY05789), while others
 CC have anti-apoptotic activity; e.g. Mrit alpha 2 (see AAY05788). Mrit
 CC alpha 1 includes an N-terminal death effector domain and a C-terminal
 CC caspase homology domain, but is not a cysteine protease. Selective
 CC enhancers and inhibitors of Mrit apoptotic activity can be identified and
 CC used to treat diseases mediated by the dysfunction of programmed cell
 CC death or proliferation. A cell accumulation disorder such as cancer,
 CC autoimmune disease, viral infection, angiogenesis or atherosclerosis is
 CC treated by administering an agent that selectively enhances Mrit
 CC apoptotic activity, thereby inducing apoptosis in a subject. A disorder
 CC of cell loss, such as a neurodegenerative disorder, including Alzheimer's
 CC disease, Parkinson's disease, retinitis pigmentosa, stroke, aplastic
 CC anemia, myocardial infarction or AIDS can be treated by administering an
 CC agent that selectively inhibits Mrit apoptotic activity
 XX
 XX Sequence 480 AA;
 SQ

Query Match 90.8%; Score 1635; DB 2; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3.6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
 QY 1 MAEIGDLKPSDVSLSIFLMKDYMGKGIKSEKSFLLDVLVELEKUNLVAPQDLLEKCL 60
 DB 97 MATIGEDLDKSDVSSLSIFLMKDYMGKGIKSEKSFLLDVLVELEKUNLVAPQDLLEKCL 156
 QY 61 KNHRIIDLTKIKYQSYQAGSTYRNVLAIOKSLKDPNNFR----- 106
 DB 157 KNHRIIDLTKIKYQSYQAGSTYRNVLAIOKSLKDPNNFR----- 216
 QY 107 ----EEPVKKSIOESAPFPOSIPPERYKMSKPLGICLIIDCIGNETELRDPTSLGY 162
 DB 217 LGAQEPVKKSIQESAPFPOSIPPERYKMSKPLGICLIIDCIGNETELRDPTSLGY 276
 DB 277 EYQKFLHSMHGISOILGFACMPHERDYSFVCVLVSRGSGSYGVQDTHSGPLPHI 336
 QY 163 EYQKFLHSMHGISOILGFACMPHERDYSFVCVLVSRGSGSYGVQDTHSGPLPHI 222
 DB 223 RRMFMGDSQPYLAGKPMFFIONVYVSDGQLEDSLSLEVDPGAMKNVFEKQKRGCLTVH 282
 DB 337 RRMFMGDSQPYLAGKPMFFIONVYVSDGQLEDSLSLEVDPGAMKNVFEKQKRGCLTVH 396
 QY 283 READFFMSJCTADMSLLEQSHSSPSLYLQCLSQKLROR 321
 DB 397 READFFMSJCTADMSLLEQSHSSPSLYLQCLSQKLROR 435
 RESULT 11
 ID AAY57454 standard; protein; 480 AA.
 XX
 XX AAY57454;
 XX
 XX 25-FEB-2000 (first entry)
 DT
 XX Human FLICE-1-like inhibitory protein long form protein sequence.
 DE
 XX Human; FLICE-1-like inhibitory protein long form; FLIP-L; FLIP-S;
 KW FLICE-1-like inhibitory protein short form; apoptosis inhibitor;
 KW atherosclerosis; vascular wall inflammation; vascular injury;
 KW Fas ligand-mediated apoptosis; atherosclerosis; transplant.
 XX
 XX Homo sapiens.
 OS
 XX
 XX W09942570-A1.
 PN
 XX 26-AUG-1999.
 PD
 PF 19-FEB-1999; 99WO-US003558.
 XX
 PR 20-FEB-1998; 98US-0075471P.
 XX
 PA (SELI-) ST ELIABETH'S MEDICAL CENT BOSTON INC.
 XX
 PI Walsh K;
 XX
 XX WPI; 1999-527469/44.
 DR N-PSDB; AAZ39040.
 XX
 XX Treating conditions characterized by vascular wall inflammation.
 PT
 XX
 XX Claim 5; Page 69-71; 105pp; English.
 PS
 XX The present sequence represents human FLICE-1-like inhibitory protein long
 CC form, designated FLIP-L. The present invention describes a new treatment
 CC of a condition characterised by vascular wall inflammation in a subject
 CC comprising administering a FLIP molecule to inhibit Fas ligand-mediated
 CC apoptosis of vascular endothelial cells in the subject. The method can be
 CC used to treat atherosclerosis, transplant arteriosclerosis and vascular
 CC injury
 XX

SQ Sequence 480 AA;
 Query Match 90.8%; Score 1635; DB 2; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3,6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

DB 1 MAEIGEDLDKSDVSLIFLMKDYMGKISKESFLDLVLEKLNVAAPQDLLEKCL 60
 97 MAEIGEDLDKSDVSLIFLMKDYMGKISKESFLDLVLEKLNVAAPQDLLEKCL 156

QY 61 KNHRIIDLKTIQKTKQSVQAGTSYRNVLOAIQKSLKDPSPNNFR----- 106
 157 KNHRIIDLKTIQKTKQSVQAGTSYRNVLOAIQKSLKDPSPNNFR----- 216

DB 107 ----EEPVKKSIOESAEFLPOSIPPEERYKMKSKPLGCLIIDICGNTELLRDTFTSLGY 162
 217 LGAQGEFVKKSIQESAEFLPOSIPPEERYKMKSKPLGCLIIDICGNTELLRDTFTSLGY 276

QY 163 EVQKFLHLSMHGISQILGQFACMPEHRDYSFVCLVSRGSGSVYGVDTSGPLPHI 222
 277 EVQKFLHLSMHGISQILGQFACMPEHRDYSFVCLVSRGSGSVYGVDTSGPLPHI 336

QY 223 RRMFMGDCPYLAGKPKKFFIIONVYVSDGLEDSLLEVDGPMKNVEFFKAQKGLCTVH 282
 337 RRMFMGDCPYLAGKPKKFFIIONVYVSDGLEDSLLEVDGPMKNVEFFKAQKGLCTVH 396

QY 283 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 321
 397 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 435

DB 397 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 435

RESULT 12
 AAY57606
 ID AAY57606 standard; protein; 480 AA.
 XX AAY57606;
 AC AAY57606;
 DT 10-MAR-2000 (first entry)
 XX 10-MAR-2000 (first entry)
 DE Human apoptosis associated protein HAPOP-1.
 XX Human; apoptosis associated protein; HAPOP; diagnosis; cytostatic;
 KW antiarteriosclerotic; antiarthritic; hepatotropic; apoptosis regulator;
 KW cell proliferative disorder; atherosclerosis; arteriosclerosis; cancer;
 KW immune disorder; rheumatoid arthritis; systemic lupus erythematosus;
 KW reproductive disorder; tumour; gastrointestinal disorder; cirrhosis;
 KW colitis; hepatitis; pancreatitis.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO99586692-A2.
 PN 18-NOV-1999.
 PD 18-NOV-1999.
 XX 11-MAY-1999; 99WO-US010386.
 PF 11-MAY-1999; 99WO-US010386.
 XX 13-MAY-1998; 98US-00078402.
 PR 13-MAY-1998; 98US-00078402.
 XX (INCY-) INCYTE PHARM INC.
 PA Hillman JL, Corley NC, Guegler KU, Patterson C, Baughn M;
 PI WPI: 2000-062303/05.
 DR N-PSDB; AAZ47926.
 XX New protein for diagnosing, treating or preventing disorders associated
 PT with increased or decreased apoptosis.
 XX Claim 1; Page 70-71; 81pp; English.
 PS The present sequence represents a human apoptosis associated protein
 CC designated HAPOP-1. HAPOP proteins are apoptosis regulators which have
 CC antiarteriosclerotic, cytostatic, antiarthritic and hepatotropic

CC activity. A pharmaceutical composition comprising HAPOP in conjunction
 CC with a carrier, a purified antagonist of HAPOP, vectors and agonists of
 CC HAPOP, are administered for diagnosing, treating or preventing disorders
 CC associated with increased or decreased apoptosis, e.g., cell proliferative
 CC disorders such as atherosclerosis, arteriosclerosis and cancers; immune
 CC disorders such as rheumatoid arthritis, systemic lupus erythematosus;
 CC reproductive disorders such as prostate cancer, endometrial and ovarian
 CC tumours; and gastrointestinal disorders such as cirrhosis, colitis,
 CC hepatitis and pancreatitis. The polynucleotides encoding HAPOP proteins
 CC may be useful to detect and quantitate expression of HAPOP genes which
 CC are correlated with diseases and are also useful to detect differences in
 CC the chromosomal location due to translocation, inversion etc., among
 CC normal, carrier, or affected individuals. The combination of the
 CC therapeutic agents may act synergistically to effect the treatment or
 CC prevention of various disorders providing improved efficacy with lower
 CC dosages of each agent and thus reducing the potential for adverse side
 CC effects

SQ Sequence 480 AA;
 Query Match 90.8%; Score 1635; DB 3; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3,6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSLIFLMKDYMGKISKESFLDLVLEKLNVAAPQDLLEKCL 60
 97 MAEIGEDLDKSDVSLIFLMKDYMGKISKESFLDLVLEKLNVAAPQDLLEKCL 156

DB 61 KNHRIIDLKTIQKTKQSVQAGTSYRNVLOAIQKSLKDPSPNNFR----- 106
 157 KNHRIIDLKTIQKTKQSVQAGTSYRNVLOAIQKSLKDPSPNNFR----- 216

QY 107 ----EEPVKKSIOESAEFLPOSIPPEERYKMKSKPLGCLIIDICGNTELLRDTFTSLGY 162
 217 LGAQGEFVKKSIQESAEFLPOSIPPEERYKMKSKPLGCLIIDICGNTELLRDTFTSLGY 276

DB 163 EVQKFLHLSMHGISQILGQFACMPEHRDYSFVCLVSRGSGSVYGVDTSGPLPHI 222
 277 EVQKFLHLSMHGISQILGQFACMPEHRDYSFVCLVSRGSGSVYGVDTSGPLPHI 336

QY 223 RRMFMGDCPYLAGKPKKFFIIONVYVSDGLEDSLLEVDGPMKNVEFFKAQKGLCTVH 282
 337 RRMFMGDCPYLAGKPKKFFIIONVYVSDGLEDSLLEVDGPMKNVEFFKAQKGLCTVH 396

QY 283 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 321
 397 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 435

DB 397 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 435

RESULT 13
 AAY67418
 ID AAY67418 standard; protein; 480 AA.
 XX AAY67418;
 AC AAY67418;
 DT 12-MAY-2000 (first entry)
 XX 12-MAY-2000 (first entry)
 DE Usurpin-alpha polypeptide.
 XX Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;
 KW usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
 KW caspase; cytostatic; antiParkinsonian; antidiabetic.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200003023-A1.
 PN 20-JAN-2000.
 PD 20-JAN-2000.
 XX 07-JUL-1999; 99WO-CA000615.
 PF 07-JUL-1999; 99WO-CA000615.
 XX 08-JUL-1998; 98US-0092005P.
 PR 08-JUL-1998; 98US-0092005P.
 XX

PA (MERI) MERCK FROST CANADA INC.
 XX
 PI Nicholson DM, Rasper DM, Xanthoudakis S, Roy S;
 XX WPI; 2000-160929/14.
 DR N-PSDB; AAZ56987.
 XX
 PT Novel recombinant DNA molecules and polypeptides for treating apoptosis
 PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
 PT disease.
 XX
 PS Claim 6; Fig 9B; 69pp; English.
 XX
 CC The invention provides recombinant nucleic acid molecules encoding
 CC usurin-alpha (lacking the first death effector domain (DED) or its
 CC prodomain), usurin-beta or usurin-gamma. Usurin polypeptides are
 CC useful for in vitro and in vivo identification of usurin-procaspase-8
 CC interaction inhibitor. Usurin is useful as modulator of the sensitivity
 CC of cells to CD95 (Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
 CC is useful for treating diseases like autoimmune diabetes, cancer and
 CC Parkinson's disease. Activators and inhibitors of usurin-procaspase-8
 CC interaction are also useful for treating various diseases mediated by
 CC apoptosis. Usurin provides an attractive model for modulating caspase
 CC activation. Sensitivity of cells bearing CD95 (Fas/Apo-1) receptor can be
 CC regulated at several levels in the presence of usurin, conferring
 CC resistance to Fas-ligand cell death. The present sequence represents the
 CC usurin-alpha polypeptide
 XX
 SO Sequence 480 AA:
 Query Match 90.8%; Score 1635; DB 3; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3.6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
 QY 1 MAEIGEDLDSDVSSLIIFLMKDYMGKISKESFLDLVVELKLNLAAPQDLLEKCL 60
 DB 97 MAEIGEDLDSDVSSLIIFLMKDYMGKISKESFLDLVVELKLNLAAPQDLLEKCL 156
 QY 61 KNHRIIDLTKIKYKQSVQAGTSYRNVLAQAIQKSLDPSNNFR----- 106
 DB 157 KNHRIIDLTKIKYKQSVQAGTSYRNVLAQAIQKSLDPSNNFR----- 106
 QY 107 -----EEPVKKSIOESAEFLPOSIPBERYKMKKPLGICIIIDICINETELLADTFTSLGY 162
 DB 217 LGAQGEFVKKSIOESAEFLPOSIPBERYKMKKPLGICIIIDICINETELLADTFTSLGY 276
 QY 163 EVQKFLHLSMHGISQILGFPACMPBEHRYDSFVCVLVSRGSGQSVYGVDOQTHSGPLPHHI 222
 DB 277 EVQKFLHLSMHGISQILGFPACMPBEHRYDSFVCVLVSRGSGQSVYGVDOQTHSGPLPHHI 336
 QY 223 RRMFMGDSCTYLAGKPMKPFIONVYVSDQLEDSSLEVDGPAMKNVFEKQKRGCLCTVH 282
 DB 337 RRMFMGDSCTYLAGKPMKPFIONVYVSDQLEDSSLEVDGPAMKNVFEKQKRGCLCTVH 396
 QY 283 READPFWSLCTADMSLLEQSHSSPSLYLOCLSOQLKQER 321
 DB 397 READPFWSLCTADMSLLEQSHSSPSLYLOCLSOQLKQER 435
 RESULT 14
 ID AAB03960 standard; protein; 480 AA.
 XX AAB03960;
 AC
 XX 26-FEB-2001 (first entry)
 XX
 DE FLICE-1-like inhibitor protein (Genbank Accession No. 2253679).
 XX
 CC Chimeric protein; fusion protein; FLICE 1-like inhibitor protein; FLIP;
 CC Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;
 CC tumour specific antigen; immune response; therapy; prophylaxis;
 CC diagnosis; HIV; human immunodeficiency syndrome; AIDS;

KY acquired immune deficiency syndrome; human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN W0200059935-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 05-APR-2000; 2000MO-US009002.
 XX
 PR 05-APR-1999; 99US-0127867P.
 PR 06-APR-1999; 99US-0128021P.
 XX
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 PA (PAPA/) PAPA C.
 PA (ALGE/) ALGECIRAS-SCHMINICH A.
 PI PAPA C, Algeciras-Schminich A;
 XX
 DR WPI; 2000-664986/64.
 XX
 PT Fusion polypeptide useful for inhibiting ligand-induced apoptosis,
 PT comprises portion of anti-apoptotic polypeptide linked to a transport
 PT group.
 XX
 PS Disclosure; Page 79-81; 89pp; English.
 XX
 CC A chimeric group or fusion peptide which comprises a portion of an anti-
 CC apoptotic polypeptide which inhibits apoptosis of lymphocytes in
 CC combination with a transport group is described. The transport group is
 CC capable of transporting the chimeric group or fusion peptide across the
 CC cell membrane. The anti-apoptotic polypeptide is FLICE-1-like inhibitor
 CC protein (FLIP) which inhibits Fas and TNF mediated apoptosis by
 CC inhibiting binding of Caspase-8 to the Fas receptor complex, thus
 CC shutting off the downstream Fas signaling pathway. The chimeric group
 CC and fusion peptide are useful for inhibiting ligand-induced apoptosis by
 CC bringing them into contact with T cells. The chimeric group is useful for
 CC expanding T cells in vitro e.g. T cells specific for particular antigens
 CC such as tumour-specific antigen, for enhancing immune response and to
 CC inhibit the apoptosis of chronically activated T cells e.g. activated
 CC CD4⁺ T cells in HIV infected patients. The chimeric group is also useful
 CC for therapeutic, prophylactic or diagnosis of intracellular delivery of
 CC small molecules and macromolecules such as anti-apoptotic polypeptides
 CC and nucleic acids encoding such polypeptides
 XX
 SO Sequence 480 AA:
 Query Match 90.8%; Score 1635; DB 3; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3.6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
 QY 1 MAEIGEDLDSDVSSLIIFLMKDYMGKISKESFLDLVVELKLNLAAPQDLLEKCL 60
 DB 97 MAEIGEDLDSDVSSLIIFLMKDYMGKISKESFLDLVVELKLNLAAPQDLLEKCL 156
 QY 61 KNHRIIDLTKIKYKQSVQAGTSYRNVLAQAIQKSLDPSNNFR----- 106
 DB 157 KNHRIIDLTKIKYKQSVQAGTSYRNVLAQAIQKSLDPSNNFR----- 106
 QY 107 -----EEPVKKSIOESAEFLPOSIPBERYKMKKPLGICIIIDICINETELLADTFTSLGY 162
 DB 217 LGAQGEFVKKSIOESAEFLPOSIPBERYKMKKPLGICIIIDICINETELLADTFTSLGY 276
 QY 163 EVQKFLHLSMHGISQILGFPACMPBEHRYDSFVCVLVSRGSGQSVYGVDOQTHSGPLPHHI 222
 DB 277 EVQKFLHLSMHGISQILGFPACMPBEHRYDSFVCVLVSRGSGQSVYGVDOQTHSGPLPHHI 336
 QY 223 RRMFMGDSCTYLAGKPMKPFIONVYVSDQLEDSSLEVDGPAMKNVFEKQKRGCLCTVH 282
 DB 337 RRMFMGDSCTYLAGKPMKPFIONVYVSDQLEDSSLEVDGPAMKNVFEKQKRGCLCTVH 396
 QY 283 READPFWSLCTADMSLLEQSHSSPSLYLOCLSOQLKQER 321

DB 397 READFWSLCTADMSLLEQSHSPSLYLQCLSQLRQER 435

RESULT 15

AB09294 ID ABB09294 strand; protein; 480 AA.

XX ABB09294;

XX 15-JUL-2002 (first entry)

DE Human FLIP-c protein SEQ ID NO:11.

XX Human; FLIP-c; caspase 8 dominant negative regulator; antiinflammatory;

XX anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;

XX phosphocholate; antisense modulation; infection; inflammation; tumour.

XX Homo sapiens.

XX WO200224717-A1.

XX 28-MAR-2002.

XX 14-SEP-2001; 2001WO-US028732.

XX 20-SEP-2000; 2000US-00666269.

XX (ISIS-) ISIS PHARM INC.

XX Ackermann EJ, Bennett CF, Zhang H, Watt AT, Rickerts W, Dean NM;

XX WPI; 2002-404948/43.

XX N-PSDB; ABL52333.

XX Novel antisense compound that hybridizes and inhibits nucleic acid

XX encoding a natural dominant negative regulator of caspase 8, FLIP-c,

XX useful for preventing or delaying infection, inflammation or tumor

XX formation.

XX Example 13; Page 118-120; 154bp; English.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX Sequence 480 AA;

XX

XX

XX

XX

XX

Query Match 90.8%; Score 1635; DB 5; Length 480;

Best Local Similarity 94.1%; Pred. No. 3; 6e-155;

Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

1 MAETGEDLDKSDVSSLLFLMKDYMGKGIKSKSFDDJVELEKINLVAPDQDLLEKCL 60

97 MAETGEDLDKSDVSSLLFLMKDYMGKGIKSKSFDDJVELEKINLVAPDQDLLEKCL 156

61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAALQKSLKDPNNFRLHNGRSKEQRLKEQ 106

DB 157 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAALQKSLKDPNNFRLHNGRSKEQRLKEQ 216

QY 107 -----EEPVKKSIOSESAFLPQSPPEBRYMKSKPGLGICLIIDCIGNETELLRDPTSLGY 162

DB 217 LGAQSEPVKKSIOSESAFLPQSPPEBRYMKSKPGLGICLIIDCIGNETELLRDPTSLGY 276

QY 163 EVQKFLHLSMHG:SQILGQFACMPEHRDYSFVCVLVSRGSGSVYGVQDTHSGLPLHI 222

DB 277 EVQKFLHLSMHG:SQILGQFACMPEHRDYSFVCVLVSRGSGSVYGVQDTHSGLPLHI 336

QY 223 RRMFMGDSCTYLAGKRMFFIQYVVSQQLDSSLLBVDGPMKNVEFKKRGCTVH 282

DB 337 RRMFMGDSCTYLAGKRMFFIQYVVSQQLDSSLLBVDGPMKNVEFKKRGCTVH 396

QY 283 READFWSLCTADMSLLEQSHSPSLYLQCLSQLRQER 321

DB 397 READFWSLCTADMSLLEQSHSPSLYLQCLSQLRQER 435

Search completed: September 8, 2004, 05:50:06

Job time : 62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:50:49 ; Search time 1037 Seconds
(without alignments)
105.731 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
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Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues
Total number of hits satisfying chosen parameters: 1298764

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|-----------------------|--------------------|
| 1 | 1800 | 100.0 | 348 | 10 US-09-009-893-6 | Sequence 6, Appl1 |
| 2 | 1800 | 100.0 | 348 | 16 US-10-713-208-6 | Sequence 6, Appl1 |
| 3 | 1635 | 90.8 | 480 | 9 US-09-861-270-2 | Sequence 2, Appl1 |
| 4 | 1635 | 90.8 | 480 | 9 US-09-410-194-11 | Sequence 11, Appl1 |
| 5 | 1635 | 90.8 | 480 | 9 US-09-410-194-17 | Sequence 17, Appl1 |
| 6 | 1635 | 90.8 | 480 | 10 US-09-009-893-2 | Sequence 2, Appl1 |
| 7 | 1635 | 90.8 | 480 | 10 US-09-471-749-1 | Sequence 1, Appl1 |
| 8 | 1635 | 90.8 | 480 | 16 US-10-713-208-2 | Sequence 2, Appl1 |
| 9 | 1630 | 90.6 | 391 | 10 US-09-764-861-37 | Sequence 37, Appl1 |
| 10 | 1630 | 90.6 | 391 | 12 US-09-764-861-37 | Sequence 37, Appl1 |
| 11 | 1630 | 90.6 | 391 | 14 US-10-103-313-318 | Sequence 318, App |
| 12 | 1630 | 90.6 | 391 | 14 US-10-115-928-37 | Sequence 37, Appl1 |
| 13 | 1579 | 87.7 | 480 | 16 US-10-408-765A-275 | Sequence 275, App |
| 14 | 1554.5 | 86.4 | 445 | 12 US-09-935-223-2 | Sequence 2, Appl1 |
| 15 | 1018 | 56.6 | 481 | 9 US-09-410-194-12 | Sequence 12, Appl1 |

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| 16 | 1018 | 56.6 | 481 | 9 US-09-410-194-19 | Sequence 19, Appl1 |
| 17 | 1006.5 | 55.9 | 484 | 13 US-10-005-821-2 | Sequence 2, Appl1 |
| 18 | 527 | 29.3 | 221 | 9 US-09-410-194-15 | Sequence 15, Appl1 |
| 19 | 527 | 29.3 | 221 | 9 US-09-410-194-22 | Sequence 22, Appl1 |
| 20 | 391 | 21.7 | 76 | 9 US-09-864-761-35073 | Sequence 35073, A |
| 21 | 313 | 17.4 | 479 | 9 US-09-410-194-20 | Sequence 20, Appl1 |
| 22 | 313 | 17.4 | 479 | 10 US-09-851-873-101 | Sequence 101, App |
| 23 | 313 | 17.4 | 479 | 15 US-10-368-438-7 | Sequence 7, Appl1 |
| 24 | 311.5 | 17.3 | 478 | 10 US-09-009-893-3 | Sequence 3, Appl1 |
| 25 | 311.5 | 17.3 | 478 | 16 US-10-713-208-3 | Sequence 3, Appl1 |
| 26 | 304.5 | 16.9 | 464 | 15 US-10-368-438-18 | Sequence 18, Appl1 |
| 27 | 304.5 | 16.9 | 496 | 12 US-10-232-884-6 | Sequence 6, Appl1 |
| 28 | 302.5 | 16.8 | 496 | 9 US-09-952-768-4 | Sequence 4, Appl1 |
| 29 | 302.5 | 16.8 | 496 | 12 US-10-668-955-4 | Sequence 4, Appl1 |
| 30 | 296.5 | 16.5 | 476 | 9 US-09-954-697-27 | Sequence 27, Appl1 |
| 31 | 277 | 15.4 | 56 | 16 US-10-627-571-5 | Sequence 7, Appl1 |
| 32 | 277 | 15.4 | 56 | 16 US-10-627-571-7 | Sequence 7, Appl1 |
| 33 | 261.5 | 14.5 | 335 | 15 US-10-368-438-16 | Sequence 16, Appl1 |
| 34 | 248.5 | 13.8 | 521 | 9 US-09-962-834A-2 | Sequence 2, Appl1 |
| 35 | 248.5 | 13.8 | 521 | 10 US-09-851-873-103 | Sequence 103, App |
| 36 | 248.5 | 13.8 | 521 | 14 US-10-439-676-2 | Sequence 2, Appl1 |
| 37 | 248.5 | 13.8 | 571 | 9 US-09-410-194-21 | Sequence 21, Appl1 |
| 38 | 244 | 13.6 | 479 | 9 US-09-952-768-2 | Sequence 2, Appl1 |
| 39 | 244 | 13.6 | 479 | 9 US-09-954-697-33 | Sequence 33, Appl1 |
| 40 | 244 | 13.6 | 479 | 10 US-09-009-893-4 | Sequence 4, Appl1 |
| 41 | 244 | 13.6 | 479 | 12 US-10-668-955-2 | Sequence 2, Appl1 |
| 42 | 244 | 13.6 | 479 | 16 US-10-713-208-4 | Sequence 4, Appl1 |
| 43 | 237 | 13.2 | 56 | 16 US-10-627-571-6 | Sequence 6, Appl1 |
| 44 | 228 | 12.7 | 286 | 9 US-09-862-915-1 | Sequence 1, Appl1 |
| 45 | 227.5 | 12.6 | 389 | 14 US-10-280-670-2 | Sequence 2, Appl1 |

ALIGNMENTS

RESULT 1
US-09-009-893-6
Sequence 6, Application US/09009893
Publication No. US20030087339A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: KENTZ, REINER J.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICP, A NOVEL INHIBITOR OF TUMOR
TITLE OF INVENTION: NEGROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,893
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488, 0970002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 348 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-009-893-6

Query Match 100.0%; Score 1800; DB 10; Length 348;
 Best Local Similarity 100.0%; Pred. No. 3, 1e-170;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQSKLKDPSNNFREEPYKKSIOESBAF 120
 QY 121 LPOSTPEERYKMKSKPLGICLIIDICGNTELLRDTFTSLGYEVQKFLHSMHGISOILG 180
 DB 121 LPOSTPEERYKMKSKPLGICLIIDICGNTELLRDTFTSLGYEVQKFLHSMHGISOILG 180
 QY 181 QFACPEHRDYSFVLCVLSRGSGQSVYGVDTQTHSGPLPHIRRMFGDSCPYLAGKPKM 240
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 DB 241 FFIQNYVSDGQLEDSSILEVDGPMKNVEFKAQKRGCLCTVHREADPFMSLCTADMSILE 300
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 DB 301 QSHSSPSLYLQCLSQKLRQERGTPGSGITTEKDMHFSSLGCTLLDVL 348

RESULT 2
 US-10-713-208-6
 Sequence 6, Application US/10713208
 Publication No. US20040121387A1
 GENERAL INFORMATION:
 APPLICANT: N1 et al.
 TITLE OF INVENTION: 1-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 at
 FILE REFERENCE: PF381C1D1
 CURRENT APPLICATION NUMBER: US/10/713,208
 PRIOR FILING DATE: 2003-11-17
 PRIOR APPLICATION NUMBER: US 09/489,155
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: US 09/009,893
 PRIOR FILING DATE: 1998-01-21
 PRIOR APPLICATION NUMBER: US 60/054,800
 PRIOR FILING DATE: 1997-08-05
 PRIOR APPLICATION NUMBER: US 60/034,205
 PRIOR FILING DATE: 1997-01-21
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 6
 LENGTH: 348
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-713-208-6

Query Match 100.0%; Score 1800; DB 16; Length 348;
 Best Local Similarity 100.0%; Pred. No. 3, 1e-170;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 121 LPOSTPEERYKMKSKPLGICLIIDICGNTELLRDTFTSLGYEVQKFLHSMHGISOILG 180
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 DB 181 QFACPEHRDYSFVLCVLSRGSGQSVYGVDTQTHSGPLPHIRRMFGDSCPYLAGKPKM 240
 QY 241 FFIQNYVSDGQLEDSSILEVDGPMKNVEFKAQKRGCLCTVHREADPFMSLCTADMSILE 300
 DB 241 FFIQNYVSDGQLEDSSILEVDGPMKNVEFKAQKRGCLCTVHREADPFMSLCTADMSILE 300
 QY 301 QSHSSPSLYLQCLSQKLRQERGTPGSGITTEKDMHFSSLGCTLLDVL 348
 DB 301 QSHSSPSLYLQCLSQKLRQERGTPGSGITTEKDMHFSSLGCTLLDVL 348

RESULT 3
 US-09-861-270-2
 Sequence 2, Application US/09861270
 Patent No. US20020052474A1
 GENERAL INFORMATION:
 APPLICANT: Su1, Hong-Bing
 TITLE OF INVENTION: Regulators of Apoptosis
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Science & Technology Law Group
 STREET: 75 Denise Drive
 CITY: Hillsborough
 STATE: California
 COUNTRY: USA
 ZIP: 94010
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/861,270
 FILING DATE: 18-May-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/795,088
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Osman, Richard A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 480 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-861-270-2

Query Match 90.8%; Score 1635; DB 9; Length 480;
 Best Local Similarity 94.1%; Pred. No. 1, 3e-153;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

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DB      277 EVOKFHLHSMHGISOILQGFACMPBHRDYSFVCVLYSRGGSQSVYGVDTQHSGLPLHHI 336
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DB      397 READFFWMSICTADMSLLEQSHSSPSLYIQCLSQKLRQER 435

RESULT 4
US-09-410-194-11
; Sequence 11, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Imleier, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-11

Query Match      90.8%; Score 1635; DB 9; Length 480;
Best Local Similarity 94.1%; Pred. No. 1,3e-153;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

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QY      61 KNHRIIDLTKTKIOKXKQSVQAGTSYRNVLQAAIOKSLKDPNNFR----- 106
DB      157 KNHRIIDLTKTKIOKXKQSVQAGTSYRNVLQAAIOKSLKDPNNFRNLNGSKQRLKEQ 216
QY      107 ----EEPVKKSIOESBAFLPQSIPEERYKMKSPKPGICLIIDICIGNETELLRDFTFTSLGY 162
DB      217 LGAQOEPRVKKSIQESBAFLPQSIPEERYKMKSPKPGICLIIDICIGNETELLRDFTFTSLGY 276

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QY      163 EVOKFHLHSMHGISOILQGFACMPBHRDYSFVCVLYSRGGSQSVYGVDTQHSGLPLHHI 222
DB      277 EVOKFHLHSMHGISOILQGFACMPBHRDYSFVCVLYSRGGSQSVYGVDTQHSGLPLHHI 336
QY      223 RRMFMGDSCEPYLAGKPKMFFIONYVVSQDQLEDSLLLEVDPAMKNVEFFKAQKGLCTVH 282
DB      337 RRMFMGDSCEPYLAGKPKMFFIONYVVSQDQLEDSLLLEVDPAMKNVEFFKAQKGLCTVH 396
QY      283 READFFWMSICTADMSLLEQSHSSPSLYIQCLSQKLRQER 321
DB      397 READFFWMSICTADMSLLEQSHSSPSLYIQCLSQKLRQER 435

RESULT 5
US-09-410-194-17
; Sequence 17, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Imleier, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-17

Query Match      90.8%; Score 1635; DB 9; Length 480;
Best Local Similarity 94.1%; Pred. No. 1,3e-153;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

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DB      97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVLVELEKLNVAPODLLEKCL 156
QY      61 KNHRIIDLTKTKIOKXKQSVQAGTSYRNVLQAAIOKSLKDPNNFR----- 106
DB      157 KNHRIIDLTKTKIOKXKQSVQAGTSYRNVLQAAIOKSLKDPNNFRNLNGSKQRLKEQ 216
QY      107 ----EEPVKKSIOESBAFLPQSIPEERYKMKSPKPGICLIIDICIGNETELLRDFTFTSLGY 162
DB      217 LGAQOEPRVKKSIQESBAFLPQSIPEERYKMKSPKPGICLIIDICIGNETELLRDFTFTSLGY 276
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DB      277 EVOKFHLHSMHGISOILQGFACMPBHRDYSFVCVLYSRGGSQSVYGVDTQHSGLPLHHI 336
QY      223 RRMFMGDSCEPYLAGKPKMFFIONYVVSQDQLEDSLLLEVDPAMKNVEFFKAQKGLCTVH 282
DB      337 RRMFMGDSCEPYLAGKPKMFFIONYVVSQDQLEDSLLLEVDPAMKNVEFFKAQKGLCTVH 396
QY      283 READFFWMSICTADMSLLEQSHSSPSLYIQCLSQKLRQER 321
DB      397 READFFWMSICTADMSLLEQSHSSPSLYIQCLSQKLRQER 435

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Db 397 READPFWSLCTADMSLLEQSHSSPSLYLQCSQKLRQER 435

RESULT 6

US-09-009-893-2
; Sequence 2, Application US/09009893
; Publication No. US20030087339A1
; GENERAL INFORMATION:
; APPLICANT: NT, JIAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: GENTZ, REINER L.
; APPLICANT: KENNY, JOSEPH J.
; TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,893
; FILING DATE: HERBWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,205
; FILING DATE: 21-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/054,800
; FILING DATE: 05-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488, 0970002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2540
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-009-893-2

Query Match 90.8%; Score 1635; DB 10; Length 480;
Best Local Similarity 94.1%; Pred. No. 1.3e-153;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGISKEKSFLDLVELEKNTLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGISKEKSFLDLVELEKNTLVAPDQDLLEKCL 156
QY 61 KNHRIIDLTKTKIQKTKQSVQAGTSYRVNLQAATQKSLKDSNNFR----- 106
DB 157 KNHRIIDLTKTKIQKTKQSVQAGTSYRVNLQAATQKSLKDSNNFRFLHNGRSKEQRLKEQ 216
QY 107 -----EPEYKKSIOSESEAFLOSIPEERYKMKSKPAGICLIDICIGNETELLADTFTSLGY 162
DB 217 LGAQCEPVKKSIOSESEAFLOSIPEERYKMKSKPAGICLIDICIGNETELLADTFTSLGY 276
QY 163 EVGQFHLHSMHGISQILGQFACMPERHDYDSFCVLSVRGSGQSVYGVVDQTHSGPLPHHI 222
DB 277 EVGQFHLHSMHGISQILGQFACMPERHDYDSFCVLSVRGSGQSVYGVVDQTHSGPLPHHI 336

QY 223 RRYFMGDSCTPYLAGKRMFFIQQNYVSDQLEDSSLLEVDGPRAMKVEFFKQKGLCTVH 282

Db 337 RRYFMGDSCTPYLAGKRMFFIQQNYVSDQLEDSSLLEVDGPRAMKVEFFKQKGLCTVH 396

QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCSQKLRQER 321

Db 397 READPFWSLCTADMSLLEQSHSSPSLYLQCSQKLRQER 435

RESULT 7

US-09-471-749-1
; Sequence 1, Application US/09471749
; Publication No. US20030124113A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/471,749
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/078,402
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0519 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TBP1PLB02
; CLONE: 157658
US-09-471-749-1

Query Match 90.8%; Score 1635; DB 10; Length 480;
Best Local Similarity 94.1%; Pred. No. 1.3e-153;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGISKEKSFLDLVELEKNTLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGISKEKSFLDLVELEKNTLVAPDQDLLEKCL 156
QY 61 KNHRIIDLTKTKIQKTKQSVQAGTSYRVNLQAATQKSLKDSNNFR----- 106
DB 157 KNHRIIDLTKTKIQKTKQSVQAGTSYRVNLQAATQKSLKDSNNFRFLHNGRSKEQRLKEQ 216
QY 107 -----EPEYKKSIOSESEAFLOSIPEERYKMKSKPAGICLIDICIGNETELLADTFTSLGY 162
DB 217 LGAQCEPVKKSIOSESEAFLOSIPEERYKMKSKPAGICLIDICIGNETELLADTFTSLGY 276

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QY 163 EVQKFLHLSMNGISQILGQFACMPBHRDYSFVCLVSRGSGSQSYGVDOQTHSGLP.LHHI 222
|
|
|
Db 277 EVQKFLHLSMNGISQILGQFACMPBHRDYSFVCLVSRGSGSQSYGVDOQTHSGLP.LHHI 336
|
|
|
QY 223 RRMFMGDSCEPYLAGKPKMFFIIONVYVSDGLEDSLLLEVDPAMKNVFFKQKRGGLCTVH 282
|
|
|
Db 337 RRMFMGDSCEPYLAGKPKMFFIIONVYVSDGLEDSLLLEVDPAMKNVFFKQKRGGLCTVH 396
|
|
|
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321
|
|
|
Db 397 READFFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 435
|
|
|
RESULT 8
US-10-713-208-2
; Sequence 2, Application US/10713208
; Publication No. US20040121387A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: I-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 an
; FILE REFERENCE: PF381C1D1
; CURRENT APPLICATION NUMBER: US/10/713,208
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US 09/489,155
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-713-208-2
Query Match 90.8%; Score 1635; DB 16; Length 480;
Best Local Similarity 94.1%; Pred. No. 1.3e-153;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVLELEKLNVAPOQLDLEKCL 60
|
|
|
Db 97 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVLELEKLNVAPOQLDLEKCL 156
|
|
|
QY 61 KNHRIIDLTKTKIOKKQSVQAGTSYRNVLOAIOKSLKDPNNFR----- 106
|
|
|
Db 157 KNHRIIDLTKTKIOKKQSVQAGTSYRNVLOAIOKSLKDPNNFRLNHNGSKQRLKEQ 216
|
|
|
QY 107 -----EEPVKKSIOESEAFLPQSIPEERYMKSKPLGICLIIDICIGNETELLDPTFTSLGY 162
|
|
|
Db 217 LGAQOEPRVKKSIQSEAFLPQSIPEERYMKSKPLGICLIIDICIGNETELLDPTFTSLGY 276
|
|
|
QY 163 EVQKFLHLSMNGISQILGQFACMPBHRDYSFVCLVSRGSGSQSYGVDOQTHSGLP.LHHI 222
|
|
|
Db 277 EVQKFLHLSMNGISQILGQFACMPBHRDYSFVCLVSRGSGSQSYGVDOQTHSGLP.LHHI 336
|
|
|
QY 223 RRMFMGDSCEPYLAGKPKMFFIIONVYVSDGLEDSLLLEVDPAMKNVFFKQKRGGLCTVH 282
|
|
|
Db 337 RRMFMGDSCEPYLAGKPKMFFIIONVYVSDGLEDSLLLEVDPAMKNVFFKQKRGGLCTVH 396
|
|
|
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321
|
|
|
Db 397 READFFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 435
|
|
|
RESULT 9
US-09-764-861-37
; Sequence 37, Application US/09764861
; Publication No. US20030171252A9
```

```
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-861-37
Query Match 90.6%; Score 1630; DB 10; Length 391;
Best Local Similarity 93.8%; Pred. No. 3.1e-153;
Matches 318; Conservative 2; Mismatches 1; Indels 18; Gaps 1;
QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVLELEKLNVAPOQLDLEKCL 60
|
|
|
Db 8 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVLELEKLNVAPOQLDLEKCL 67
|
|
|
QY 61 KNHRIIDLTKTKIOKKQSVQAGTSYRNVLOAIOKSLKDPNNFR----- 106
|
|
|
Db 68 KNHRIIDLTKTKIOKKQSVQAGTSYRNVLOAIOKSLKDPNNFRLNHNGSKQRLKEQ 127
|
|
|
QY 107 -----EEPVKKSIOESEAFLPQSIPEERYMKSKPLGICLIIDICIGNETELLDPTFTSLGY 162
|
|
|
Db 128 LGAQOEPRVKKSIQSEAFLPQSIPEERYMKSKPLGICLIIDICIGNETELLDPTFTSLGY 187
|
|
|
QY 163 EVQKFLHLSMNGISQILGQFACMPBHRDYSFVCLVSRGSGSQSYGVDOQTHSGLP.LHHI 222
|
|
|
Db 188 EVQKFLHLSMNGISQILGQFACMPBHRDYSFVCLVSRGSGSQSYGVDOQTHSGLP.LHHI 247
|
|
|
QY 223 RRMFMGDSCEPYLAGKPKMFFIIONVYVSDGLEDSLLLEVDPAMKNVFFKQKRGGLCTVH 282
|
|
|
Db 248 RRMFMGDSCEPYLAGKPKMFFIIONVYVSDGLEDSLLLEVDPAMKNVFFKQKRGGLCTVH 307
|
|
|
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321
|
|
|
Db 308 READFFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 346
|
|
|
RESULT 10
US-09-764-861-37
; Sequence 37, Application US/09764861
; Publication No. US20020086811A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-861-37
Query Match 90.6%; Score 1630; DB 12; Length 391;
Best Local Similarity 93.8%; Pred. No. 3.1e-153;
```

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Matches 318; Conservative 2; Mismatches 1; Indels 18; Gaps 1;
QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKESFLDLVLEKLNVAAPDQDLLEKCL 60
DB 8 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKESFLDLVLEKLNVAAPDQDLLEKCL 67
QY 61 KNHRIIDLTKTIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
DB 68 KNHRIIDLTKTIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRFLHNGRSKQRLKEQ 127
QY 107 ----EBPVKSIQSEAFIPQSIPEERYKMKSKPLGICIIDICIGNETELLRDFTSLGY 162
DB 128 LGAQGEPPVKSIQSEAFIPQSIPEERYKMKSKPLGICIIDICIGNETELLRDFTSLGY 187
QY 163 EVQKFLHLSMHGISQILGQFACMPERHDYDSFVCVLSRGSQSVYGVDTHTSGLPPLHHI 222
DB 188 EVQKFLHLSMHGISQILGQFACMPERHDYDSFVCVLSRGSQSVYGVDTHTSGLPPLHHI 247
QY 223 RRMFMGDSCPYLAKGPKMFFIQNYVVSQGLEDSLSLEVDGPAKKNVEFKAKQKGLCTVH 282
DB 248 RRMFMGDSCPYLAKGPKMFFIQNYVVSQGLEDSLSLEVDGPAKKNVEFKAKQKGLCTVH 307
QY 283 READFFWMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
DB 308 READFFWMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 346

RESULT 11
US-10-103-313-318
; Sequence 318, Application US/10103313
; Publication No. US20030082756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1207C1
; CURRENT APPLICATION NUMBER: US/10/103.313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 318
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (97)_feature
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-318

Query Match 90.6%; Score 1630; DB 14; Length 391;
Best Local Similarity 93.8%; Pred. No. 3.1e-153;
Matches 318; Conservative 2; Mismatches 1; Indels 18; Gaps 1;
QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKESFLDLVLEKLNVAAPDQDLLEKCL 60
DB 8 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKESFLDLVLEKLNVAAPDQDLLEKCL 67
QY 61 KNHRIIDLTKTIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
DB 68 KNHRIIDLTKTIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRFLHNGRSKQRLKEQ 127
QY 107 ----EBPVKSIQSEAFIPQSIPEERYKMKSKPLGICIIDICIGNETELLRDFTSLGY 162
DB 128 LGAQGEPPVKSIQSEAFIPQSIPEERYKMKSKPLGICIIDICIGNETELLRDFTSLGY 187
QY 163 EVQKFLHLSMHGISQILGQFACMPERHDYDSFVCVLSRGSQSVYGVDTHTSGLPPLHHI 222
DB 188 EVQKFLHLSMHGISQILGQFACMPERHDYDSFVCVLSRGSQSVYGVDTHTSGLPPLHHI 247
QY 223 RRMFMGDSCPYLAKGPKMFFIQNYVVSQGLEDSLSLEVDGPAKKNVEFKAKQKGLCTVH 282
DB 248 RRMFMGDSCPYLAKGPKMFFIQNYVVSQGLEDSLSLEVDGPAKKNVEFKAKQKGLCTVH 307
```

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QY 283 READFFWMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
DB 308 READFFWMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 346

RESULT 12
US-10-115-928-37
; Sequence 37, Application US/10115928
; Publication No. US20030092615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1204C1
; CURRENT APPLICATION NUMBER: US/10/115.928
; CURRENT FILING DATE: 2002-04-05
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (97)_feature
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-115-928-37

Query Match 90.6%; Score 1630; DB 14; Length 391;
Best Local Similarity 93.8%; Pred. No. 3.1e-153;
Matches 318; Conservative 2; Mismatches 1; Indels 18; Gaps 1;
QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKESFLDLVLEKLNVAAPDQDLLEKCL 60
DB 8 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKESFLDLVLEKLNVAAPDQDLLEKCL 67
QY 61 KNHRIIDLTKTIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
DB 68 KNHRIIDLTKTIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRFLHNGRSKQRLKEQ 127
QY 107 ----EBPVKSIQSEAFIPQSIPEERYKMKSKPLGICIIDICIGNETELLRDFTSLGY 162
DB 128 LGAQGEPPVKSIQSEAFIPQSIPEERYKMKSKPLGICIIDICIGNETELLRDFTSLGY 187
QY 163 EVQKFLHLSMHGISQILGQFACMPERHDYDSFVCVLSRGSQSVYGVDTHTSGLPPLHHI 222
DB 188 EVQKFLHLSMHGISQILGQFACMPERHDYDSFVCVLSRGSQSVYGVDTHTSGLPPLHHI 247
QY 223 RRMFMGDSCPYLAKGPKMFFIQNYVVSQGLEDSLSLEVDGPAKKNVEFKAKQKGLCTVH 282
DB 248 RRMFMGDSCPYLAKGPKMFFIQNYVVSQGLEDSLSLEVDGPAKKNVEFKAKQKGLCTVH 307
QY 283 READFFWMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
DB 308 READFFWMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 346

RESULT 13
US-10-408-765A-275
; Sequence 275, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Robin D.
; APPLICANT: Zhand, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
```


CURRENT APPLICATION NUMBER: US/10/409,765A
 CURRENT FILING DATE: 2003-04-04
 NUMBER OF SEQ ID NOS: 3077
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 275
 LENGTH: 480
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-10-408-765A-275

Query Match 87.7%; Score 1579; DB 16; Length 480;
 Best Local Similarity 91.2%; Pred. No. 5,1e-148;
 Matches 309; Conservative 4; Mismatches 8; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSLIFLMKDYMGKGIKSKESFLDVLVELEKLNVAPODLLEKCL 60
 DB 97 MAEIGEDLDKSDVSLIFLMKDYMGKGIKSKESFLDVLVELEKLNVAPODLLEKCL 156
 QY 61 KNHRIIDLTKIKQKYSVQAGTSYRNVLOAIOKSLKDPNNR----- 106
 DB 157 KNHRIIDLTKIKQKYSVQAGTSYRNVLOAIOKSLKDPNNRFLHNGSKESQRLKEQ 216
 QY 107 -----EEPVKKSIOESAPLPOSIPERRYKSKPLGICLIIDICIGNETELLADPTFTSLGY 162
 DB 217 LGAQDEPVKKSIOESAPLPOSIPERRYKSKPLGICLIIDICIGNETELLADPTFTSLGY 276
 QY 163 EVQKFLHLSHGISOILGQFACMPEHRDYSFVCVLVSRGSGSVYGVDTSHGLPLHHI 222
 DB 277 EVQKFLHLSHGISOILGQFACMPEHRDYSFVCVLVSRGSGSVYGVDTSHGLPLHHI 336
 QY 223 RMFMGDSCEPYLAGKRPFFIIONVYVSDGLDESSLEVDGPMKNVFFKQKRGCLTVH 282
 DB 337 RMFMGDSCEPYLAGKRPFFIIONVYVSDGLDESSLEVDGPMKNVFFKQKRGCLTVH 396
 QY 283 READPFMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
 DB 397 READPFMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 14
 US-09-935-223-2
 ; Sequence 2, Application US/09935223
 ; Publication No. US20020086983A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alameda, Emaad S.
 ; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, Ar
 ; FILE REFERENCE: T02499
 ; CURRENT APPLICATION NUMBER: US/09/935,223
 ; CURRENT FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 09/723,450
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 09/276,993
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 08/859,167
 ; PRIOR FILING DATE: 1997-05-20
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 445
 ; TYPE: PRF
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Novel Sequence
 US-09-935-223-2

Query Match 86.4%; Score 1554.5; DB 12; Length 445;
 Best Local Similarity 94.4%; Pred. No. 1.2e-145;
 Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;
 QY 1 MAEIGEDLDKSDVSLIFLMKDYMGKGIKSKESFLDVLVELEKLNVAPODLLEKCL 60
 DB 97 MAEIGEDLDKSDVSLIFLMKDYMGKGIKSKESFLDVLVELEKLNVAPODLLEKCL 156

QY 61 KNHRIIDLTKIKQKYSVQAGTSYRNVLOAIOKSLKDPNNRFPREPVKKSIOESAP 120
 DB 157 KNHRIIDLTKIKQKYSVQAGTSYRNVLOAIOKSLKDPNNR----- 202
 QY 121 LPQSIPEERYKMSKPLGICLIIDICIGNETELLADPTFTSLGYEQKFLHSMHISOILG 180
 DB 203 ---SIPEERYKMSKPLGICLIIDICIGNETELLADPTFTSLGYEQKFLHSMHISOILG 259
 QY 181 QFACMPEHRDYSFVCVLVSRGSGSVYGVDTSHGLPLHHIRMFMGDSCEPYLAGKPKM 240
 DB 260 QFACMPEHRDYSFVCVLVSRGSGSVYGVDTSHGLPLHHIRMFMGDSCEPYLAGKPKM 319
 QY 244 FFIQNVYVSDGLEPSSSLEVDGPMKNVFFKQKRGCLTVHREADPFMSLCTADMSLLE 300
 DB 320 FFIQNVYVSDGLEPSSSLEVDGPMKNVFFKQKRGCLTVHREADPFMSLCTADMSLLE 379
 QY 301 QSHSSEPSLYLQCLSQKLRQER 321
 DB 380 QSHSSEPSLYLQCLSQKLRQER 400

RESULT 15
 US-09-410-194-12
 ; Sequence 12, Application US/09410194
 ; Patent No. US20020095030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tschopp, Jurg
 ; APPLICANT: Thome, Margot
 ; APPLICANT: Burns, Kimberly
 ; APPLICANT: Imtler, Marten
 ; APPLICANT: Hahne, Michael
 ; APPLICANT: Schroter, Michael
 ; APPLICANT: Schneider, Pascal
 ; APPLICANT: Bodmer, Jean-Luc
 ; APPLICANT: Steiner, Veronique
 ; APPLICANT: Rimoldi, Denata
 ; APPLICANT: Holmann, Kay
 ; APPLICANT: French, E. Lars
 ; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
 ; FILE REFERENCE: 11141-002001
 ; CURRENT APPLICATION NUMBER: US/09/410,194
 ; CURRENT FILING DATE: 1999-09-30
 ; PRIOR APPLICATION NUMBER: PCT/EP98/01857
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: GERMAN 197 13 393.2
 ; PRIOR FILING DATE: 1997-04-01
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 481
 ; TYPE: PRF
 ; ORGANISM: Mus musculus
 US-09-410-194-12

Query Match 56.6%; Score 1018; DB 9; Length 481;
 Best Local Similarity 62.6%; Pred. No. 3.6e-92;
 Matches 211; Conservative 41; Mismatches 67; Indels 18; Gaps 5;

QY 1 MAEIGEDLDKSDVSLIFLMKDYMGKGIKSKESFLDVLVELEKLNVAPODLLEKCL 60
 DB 102 LMEIGSIDQNDVSLVFLTRDYGRKIAKDSFLDVLVELEKLNVAPODLLEKCL 161
 QY 61 KNHRIIDLTKIKQKYSVQAGTSYRNVLOAIOKSLKDPNNR----- 109
 DB 162 KNHRIIDLTKIKQKYSVQAGTSYRNVLOAIOKSLKDPNNRFLHNGSKESQRLKEQ 216
 QY 110 -----VKKSIOESAPLPOSIPERRYKMSKPLGICLIIDICIGNETELLADPTFTSLGYEV 164
 DB 221 SQRTLVKHSIOESGAFPLPHIREIRYMQSKPLGICLIIDICIGNDTVLQETFTSLGYHI 280
 QY 165 QKFLHLSHGISOILGQFACMPEHRDYSFVCVLVSRGSGSVYGVDTSHGLPLHHIR 224

| | | | |
|----|-----|---|-----|
| Db | 281 | QLFLPKSHDITQIVRRYASMAQHODYDSFACVLVSLGSGQSMGRDQVHSGPSLDHYKN | 340 |
| Qy | 225 | MEMDSCPYLAGKPKMFFIONYYVSDGLEDDSSILEVDGPAMKNVEFKAQKRGCTVHRE | 284 |
| Db | 341 | MFTGDTCPSLRGKPKLFFIQNYESLGSQLEDDSS-LEVDPSPINVDKPLQPRHCTTHPE | 399 |
| Qy | 285 | ADFFMSLCTADMSLLEQSHSPSLYLQCLSOXLROR | 321 |
| Db | 400 | ADFFMSLCTADVSHLEKPSSSSVYLOKLSQULKQGR | 436 |

Search completed: September 8, 2004, 06:22:25
Job time : 1043 secs

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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:48:38 ; Search time 19 Seconds
(without alignments)
1761.824 Million cell updates/sec

Title: US-10-713-208-6

Perfect score: 1800
Sequence: 1 MA1G6DLKSDVSLIFLM.....ITRSKDMFSSUGLILDLVL 348

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 184.5 | 10.2 | 212 | 2 167437 | cysteine proteinase |
| 2 | 184.5 | 10.2 | 277 | 2 S64710 | cysteine proteinase |
| 3 | 184.5 | 10.2 | 277 | 2 CPJ32 | CPJ32 protein - mo |
| 4 | 183.5 | 10.2 | 277 | 2 A55315 | cysteine proteinase |
| 5 | 180.5 | 10.0 | 452 | 2 JC6507 | caspase-2 - rat |
| 6 | 177.5 | 9.9 | 435 | 2 A54821 | apoptosis regulato |
| 7 | 169 | 9.4 | 312 | 2 B54821 | apoptosis regulato |
| 8 | 161 | 8.9 | 416 | 2 G02635 | ICB-LAB6 - human |
| 9 | 149.5 | 8.3 | 182 | 2 167436 | interleukin-1-beta |
| 10 | 138.5 | 7.7 | 418 | 2 B57311 | interleukin-1-beta |
| 11 | 136 | 7.6 | 383 | 2 A56084 | interleukin-1-beta |
| 12 | 134 | 7.4 | 454 | 2 TC7123 | caspase-9 long cha |
| 13 | 129.5 | 7.2 | 495 | 2 T20038 | hypothetical prote |
| 14 | 129.5 | 7.2 | 503 | 2 A49429 | interleukin-1 beta |
| 15 | 126.5 | 7.0 | 404 | 2 A42677 | interleukin-1 beta |
| 16 | 124.5 | 6.9 | 311 | 2 B56084 | interleukin-1-beta |
| 17 | 122 | 6.8 | 241 | 2 T30761 | hypothetical prote |
| 18 | 120 | 6.7 | 263 | 2 C56084 | interleukin-1-beta |
| 19 | 116 | 6.4 | 377 | 2 A57511 | interleukin-1 beta |
| 20 | 109.5 | 6.1 | 402 | 2 A46495 | IL-1 beta converta |
| 21 | 102 | 5.7 | 1537 | 2 F86509 | CT147 hypothetical |
| 22 | 102 | 5.7 | 1537 | 2 C81558 | conserved hypothet |
| 23 | 102 | 5.7 | 1537 | 2 H72112 | ct147 hypothetical |
| 24 | 101.5 | 5.6 | 743 | 2 G83726 | assimilatory nitra |
| 25 | 100 | 5.6 | 1819 | 2 A71928 | cag island protein |
| 26 | 98.5 | 5.5 | 613 | 2 A99552 | oligoendopeptidase |
| 27 | 98.5 | 5.5 | 680 | 2 T41670 | hypothetical zinc |
| 28 | 98.5 | 5.5 | 1641 | 2 T10955 | early nodulin bind |
| 29 | 97.5 | 5.4 | 854 | 2 C83905 | hypothetical prote |

| | | | | | |
|----|------|-----|------|----------|--------------------|
| 30 | 97.5 | 5.4 | 2104 | 2 T18774 | myosin-3 heavy cha |
| 31 | 97 | 5.4 | 892 | 2 A61661 | transcription regu |
| 32 | 96.5 | 5.4 | 1287 | 2 T42658 | hypothetical prote |
| 33 | 96 | 5.3 | 488 | 2 T13385 | hypothetical prote |
| 34 | 95 | 5.3 | 892 | 2 A11289 | transcription regu |
| 35 | 95 | 5.3 | 1629 | 2 T06461 | DNA-binding protei |
| 36 | 94.5 | 5.2 | 344 | 2 B70136 | flagellar motor sw |
| 37 | 94 | 5.2 | 1713 | 2 A55347 | adhesive ligand ep |
| 38 | 94 | 5.2 | 2670 | 2 A46719 | inositol 1,4,5-tri |
| 39 | 94 | 5.2 | 2671 | 2 A46873 | inositol 1,4,5-tri |
| 40 | 94 | 5.2 | 4589 | 2 T14914 | dynein beta heavy |
| 41 | 93.5 | 5.2 | 1811 | 2 T39252 | probable protein t |
| 42 | 93 | 5.2 | 455 | 2 G70113 | replicative DNA he |
| 43 | 93 | 5.2 | 1265 | 2 T47626 | structural mainten |
| 44 | 93 | 5.2 | 1675 | 2 S38173 | myosin-like protei |
| 45 | 93 | 5.2 | 1927 | 2 G64585 | cag pathogenicity |

ALIGNMENTS

RESULT 1

167437
cysteine proteinase (EC 3.4.22.-) p32 - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

C/Accession: 167437

R/Flaws: J.A.; Kugu. K.; Trbovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfield, A.N.; Til

A/Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel

nulosa cells of the ovarian follicle

A/Reference number: 153300; PMID:96042508; PMID:7588240

A/Accession: 167437

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1212 <RES>

A/Cross-references: EMBL:U34685; NID:91004370; PIDN:AAC52251.1; PID:91004371

C/Keywords: cysteine proteinase; hydrolase

Query Match 10.2%; Score 184.5; DB 2; Length 212;
Best Local Similarity 29.1%; Pred. No. 7.2e-07;
Matches 60; Conservative 36; Mismatches 81; Indels 29; Gaps 8;

| | | |
|--|-----|--|
| QY | 127 | EEHYKMKSRPLGICLLID-----CIGNETEL---LRDTFTSLGYEQKRLHISM 172 |
| DB | 5 | DSSEYKMDYDEMGLCIINNNKFNHSTGMSARRNGTVDANLRETFWALKYEVRNNNDLIR 64 |
| QY | 173 | HGISOILGCPACPEHRDYDSFVCVLVSRGSGSYGVQDTHSGPLHHRIRMFWDSCP 232 |
| DB | 65 | EEIMELMDSVS-KEDSKSSSFVCVILSHGDEGVIFG---TNGPVDIKKLISFFRGDYCR 120 |
| QY | 233 | YLAKPRMFFIQLYVVSQQLDESDLSLEVDPKMKNVFEKAKRGCLTVHRRADFFWSLC 292 |
| DB | 121 | SLTGKPKLFLFIQ---ACRGTELDPSG-IETDSGADDDV--ACCKGKV-----EADFLVAYS 169 |
| QY | 293 | TADMSLLEQSHSSPSLYLQCLSGKLR 318 |
| DB | 170 | SAPGYISWRNSRGSGSWFIQSLCMLK 195 |
| RESULT 2 | | |
| S64710 | | |
| cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster | | |
| C/Species: Citellus griseus (Chinese hamster) | | |
| C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999 | | |
| C/Accession: S64710; S72395 | | |
| R/Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L. | | |
| EMBO J. 15, 1012-1020, 1996 | | |
| A/Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during | | |
| A/Reference number: S64710; PMID:96183185; PMID:8605870 | | |
| A/Accession: S64710 | | |
| A/Status: nucleic acid sequence not shown | | |
| A/Molecule type: mRNA | | |

A:Residues: 1-277 <MAN>
 A:Cross-references: EMBL:U07463
 R:Wang, X.
 Submitted to the EMBL Data Library, May 1995
 A:Reference number: S72395
 A:Accession: S72395
 A:Molecule type: mRNA
 A:Residues: 1-79, 'A', 81-146, 'Y', 148-277 <MAN>
 A:Cross-references: EMBL:U07463; NID:G244443; PIDD:AA01511.1; PID:G244444
 C:Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 10.2%; Score 184.5; DB 2; Length 277;
 Best Local Similarity 27.9%; Pred. No. 1e-06;
 Matches 67; Conservative 36; Mismatches 94; Indels 43; Gaps 9;

QY 96 KSLKPPNNPREPYKKS-IOESFAFLPQSIPEERYKSKKPLGICLIID----- 144
 DB 11 KSIK---NFEVKTIHSGSKSMDSGIYLDSS---YKMDYPENGVCIINNNKPKHKTGM 61
 QY 145 --CIGNETEL--LRDFTSLGYEVOKFLHSMHGISOILGQFACMPERHDYDFVCVLS 200
 DB 62 TPRSTVDPAKLETETFNALKYEVANKNDLREIIVELM-KAKSKEDHKSRSFVCVILS 120
 QY 201 RGGSSQVYGVQDTHSGPLHHRFMWGDSCPYLAGKPKKFFIQ--NYVSDGQLEDSSL 258
 DB 121 HGBEGVIFGTD---GPIDLKLTGYFRGDCRSLSIGKPKLFIQACRGTELDGIEITDSG 177
 QY 259 LEVDGPAKKNVEFKAQKGLCTVHREADFMSLCTADMSLLEQSHSPSLYICQCSQKLR 318
 DB 178 TEDMTCK-----IPEVADFLYAVSTAGYYSWRNPKDGSWFIQSLCSMLK 224

RESULT 3
 JC5410
 C:P32 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
 C:Accession: JC5410
 R:Murakami, T.; Urase, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
 Biochem. Biophys. Res. Commun. 231, 770-774, 1997
 A:Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation
 A:Reference number: JC5410; MUID:97224429; PMID:9070890
 A:Accession: JC5410
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-277 <MDK>
 A:Cross-references: DDBJ:D86352
 A:Experimental source: embryo
 C:Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 10.2%; Score 184.5; DB 2; Length 277;
 Best Local Similarity 28.9%; Pred. No. 1e-06;
 Matches 67; Conservative 35; Mismatches 93; Indels 37; Gaps 11;

QY 103 NNPREPY--KKSIOESFAFLPQSIPEERYKSKKPLGICLIIT-----DCIGN 148
 DB 14 NNFGVKTTHGSKSV-DSGIYLDSS---YKMDYPENGVCIITNNKPKHKTGMSSRSST 67
 QY 149 ETEL--LRDFTSLGYEVOKFLHSMHGISOILGQFACMPERHDYDFVCVLSRGGSS 206
 DB 68 DVDANLREITFMGLKYEVANKNDLREIIVELMDSVS-KEDHKSRSFVCVILSHGDEGV 126
 QY 207 VYGVQDTHSGPLHHRFMWGDSCPYLAGKPKKFFIQNVVSDGQLEDSSLLEVDGPM 266
 DB 127 IFG---TNGPVDLKKLTSPFRGDYCRSLTGKPKLFIITQ--ACRGTELDG--IETDSGT- 178
 QY 267 KNEFKAQKGLCTVHREADFMSLCTADMSLLEQSHSPSLYICQCSQKLR 318
 DB 179 -DEMAQCK-----IPEVADFLYAVSTAGYYSWRNPKDGSWFIQSLCSMLK 224

RESULT 4
 A55315

cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human

N:Alternate names: cysteine proteinase CPP32
 C:Species: Homo sapiens (man)
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
 C:Accession: A55315; S58899; I39005
 R:Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
 J. Biol. Chem. 269, 30761-30764, 1994

A:Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans
 A:Reference number: A55315; MUID:95074098; PMID:7983002
 A:Accession: A55315
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-277 <FPR>

A:Cross-references: GB:U13737; NID:G561665; PIDD:AA65015.1; PID:G561666
 R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Viallancourt, J.P.; Ding, C.K.; Gallant,
 J.; Yu, V.L.; Miller, D.K.
 Nature 376, 37-43, 1995

A:Title: Identification and inhibition of the ICE/CED-3 protease necessary for mamma
 A:Reference number: S58899; MUID:95319529; PMID:7596430
 A:Accession: S58899
 A:Molecule type: protein

A:Residues: 29-46, 176-189, 'E', 191-193 <NIC>
 R:Revard, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poit
 Cell 81, 801-809, 1995

A:Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
 A:Reference number: A56924; MUID:95292347; PMID:7774019
 A:Accession: I39005
 A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-189, 'E', 191-277 <RES>
 A:Cross-references: EMBL:U06943; NID:G857568; PIDD:AAV4929.1; PID:G857569
 C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 10.2%; Score 183.5; DB 2; Length 277;
 Best Local Similarity 26.4%; Pred. No. 1.2e-06;
 Matches 64; Conservative 41; Mismatches 100; Indels 37; Gaps 7;

QY 98 LKDPNNPREPYK---KSIOESFAFLPQSIPEERYKSKKPLGICLIID----- 144
 DB 1 MENTENSVMVSKSKIKNLEPKTIHSGESMDSGISLDNSYKMDYPEMGLCIINNNKPKHKTG 60
 QY 145 ---CIGNETEL--LRDFTSLGYEVOKFLHSMHGISOILGQFACMPERHDYDFVCVLY 199
 DB 61 MTRSGTDVPAKLETETFNALKYEVANKNDLREIIVELMDSVS-KEDHKSRSFVCVIL 119
 QY 200 SRGSSQVYGVQDTHSGPLHHRFMWGDSCPYLAGKPKKFFIQ--NYVSDGQLEDSS 257
 DB 120 SHGBEGIFG---TNGPVDLKKLTNPFREDRCRSLTGKPKLFIQACRGTELDGIEITDS 176
 QY 258 LLEVDGPAKKNVEFKAQKGLCTVHREADFMSLCTADMSLLEQSHSPSLYICQCSQKLR 317
 DB 177 GVDDDMACHK-----IPEVADFLYAVSTAGYYSWRNPKDGSWFIQSLCSML 223
 QY 318 RQ 319
 DB 224 KQ 225

RESULT 5
 JC6507
 Caspase-2 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: JC6507
 R:Saco, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
 Gene 202, 127-132, 1997
 A:Title: Cloning and expression of the cDNA encoding rat caspase-2.
 A:Reference number: JC6507; MUID:98087427; PMID:9427555
 A:Accession: JC6507
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-452 <SAT>
 A:Cross-references: GB:U07933; NID:G2769705; PIDD:AA096379.1; PID:G2769706

```

Db      263 EGATGYVD--GKLLQIQEYFQLEFDNANCSLQNKPKMFIIQ---ACRGDETGRGVQDQG 317
QY      264 -----PANKVNEFKQKRGKGLCTVHREADPFMSLCIADMSLLEQSSSPSLVQGLCSQ-- 315
Db      318 KKHAGSPGCEESDAGEKELPKRMELPTRSDMICGYACLKCTAARNRYKRSWYTEALQYV 377
QY      316 -----KLQERGTIPSGSITESKDM 335
Db      378 SERACDMVADMVKYNALIKOREGYAPGTETFRCKEM 415

RESULT 7
apoptosis regulator ICH-1, suppressive form S - human
B54821
C:Species: Homo sapiens (man)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C:Accession: B54821
R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994
A:Title: Ich-1, an I $\kappa$ B/c $\kappa$ B-3-related gene, encodes both positive and negative regulators
A:Reference number: A54821; MUID:94373811; PMID:8087842
A:Accession: B54821
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-312 <MAN>
A:Cross-references: GB:U10322
C:Keywords: alternative splicing; apoptosis

Query Match          9.4%; Score 169; DB 2; Length 312;
Best Local Similarity 23.5%; Pred. No. 1,9e-05;
Matches 66; Conservative 45; Mismatches 90; Indels 80; Gaps 9;

QY      42 LEKNTLVAPDQL--DLLEKCL-KNIHRIIDLK--TKIQKYQSYQAGACTSYRNLQA- 92
Db      9 LKKNRVYLAQKLLSELLEHLEKDIITLEMRELQAKVGSFQNVELLNLPRKGPQAF 68
QY      93 -AQKSLKQDSNNFRREPVKKSIQSENAFLP-----QSTP----- 126
Db      69 DAFCEALRETKQGHLEDMLTITLSGLQHVLPUSCDYDSLPPVGCSCPLYKKRLSTD 128
QY      127 -----EERYKMSKPLGICLIIDCI--GNETEL-- 152
Db      129 TVEHSIDNKGDPVCLQKPCPTPEFYQTHPQLAVLRQSRPGLALVLSNVHFTGEKELEFR 188
QY      153 -----LRDFTSLGIEYVQKFLHLSMHGISQIIGQFPCMCPEHNDYDSFCVLYSRGG 203
Db      189 SGGDVHSTLVTLVFLKLGVDVHVLCDQTAGEMERKIQNFQQLPAHRAVTSICVALLSHGV 248
QY      204 SOSVYGVDQTHSGPLPHIRRMFGDSCPYLAKPKMFFIQ 244
Db      249 EGATGYVD--GKLLQIQEYFQLEFDNANCSLQNKPKMFIIQ 287

RESULT 8
ICH-LAP6 - human
G02635
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: G02635
R:Duan, H.; Orth, K.; Chinaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,
submitted to the EMBL Data Library, April 1996
A:Reference number: H01513
A:Accession: G02635
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-416 <DUA>
A:Cross-references: EMBL:U56390; NID:g1336026; PIDN:AA05640.1; PID:g1336027

Query Match          8.9%; Score 161; DB 2; Length 416;
Best Local Similarity 22.0%; Pred. No. 0.00011;
Matches 77; Conservative 60; Mismatches 149; Indels 64; Gaps 11;

QY      19 LMDYMGKGISKEKSLDVLVELEKNTLVAPDQDLLEKCLKNIHRIIDLTKIQKTKQS 78

```

Db 39 MIEDIQRAGSGSRDQARQLIIDLETGSOA---LPFLISCLDITQDVLASTLRTRRQA 95
Qy 79 VQAGTGYRNLQAIQKSLKDP-----SNFREPYPKKSIOSEAFPLPQS 124
Db 96 GKLSTKPTLENLTPVLRREIKRPVLRPEPRPVDSGGFGVGLSELRGN----- 148
Qy 125 IPEERYKKSKPLGICLIIDCTG--NTELLRDTFTSLGYEVQKPLHLHMEGISQILGCF 182
Db 149 ADLAVYILSMPEPCGCHLNNVNCRESGLRTRGNSIDEXKRRRFRSSLHFVEVYKIDL 207
Qy 153 A-----CMPEHRDYSFVCLVSRGSGQS-----YGVDTQTHSGLP--LHHI 222
Db 208 TAKKNVLLBELAQDHGALDCCVAVILSHGCQASHLQFPAVYGTD---GCPVSEVKI 263
Qy 223 RRMFKGDCPYLAGKPKMFTIQ-----NYVSDGQLED---SLLSEVDG-PAMKNV 269
Db 264 VNIFGTSCPSLIGKPKPLFIQACGGEQKHGEFVASTPDEBSPGSPNEPDATPFOGL 323
Qy 270 EFKQKRGCLTVHREADPFMSLCTADMSLLEQSHSSSLYLOCLSQKLO 319
Db 324 RFPDQDAISSLPSPDIFVYSYTFPGFVSMRDPKSGSWYETLDDIFEQ 373

RESULT 9

Interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C/Accession: 167436
R/Flaws, J.A.; Kugyu, K.; Tirovich, A.M.; Desanti, A.; Tilly, K.I.; Harsfield, A.N.; Tili
Endocrinology 136, 5042-5053, 1995
A/Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
lulosa cells of the ovarian follicle
A/Reference number: 153300; MUID:96042508; PMID:7586240
A/Accession: 167436
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-182 <RES>
A/Cross-references: EMBL:U34684; NID:g1004368; PIDN:AAC52260.1; PID:g1004369

Query Match 8.3%; Score 149.5; DB 2; Length 182;

Best Local Similarity 31.0%; Pred. No. 0.00028;

Matches 44; Conservative 18; Mismatches 61; Indels 19; Gaps 4;

Qy 136 PLGICLIIDCI-----GNFTE--LLRDTFTSGYEVQKPLHLSMGISQILQ 181
Db 1 PRGLALVMSNVHFTGEKDLFRSGGDVDTHTLVTLFYLQYNNHVLVYDQTAGEMEKLN 60
Qy 182 PACPEHRDYSFVCLVSRGSGSYGVDTQTHSGLPHLHIREMGDCSPYLAGKPKMF 241
Db 61 FAQIPARHVTDSCTVALSHSGVEGIGYVD--GKLQLOHVFPLFDNANCPSLONKPKMF 118
Qy 242 FIONVYVSDGLEDSLLEVDG 263
Db 119 FIQ--ACRGDETREGVDQDG 137

RESULT 10

B57511
Interleukin-1 beta converting enzyme (EC 3.4.22.-) ICE-rel-III - human
C/Species: Homo sapiens (man)
C/Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 01-Dec-2000
C/Accession: B57511; S62183
R/Munday, N.A.; Vaillancourt, J.P.; Ali, A.; Casano, F.J.; Miller, D.K.; Mollineux, S.M.
J. Biol. Chem. 270, 15870-15876, 1995
A/Title: Molecular cloning and pro-apoptotic activity of ICE-relIII and ICE-relIII, membe
r A/Reference number: A57511; MUID:95318183; PMID:7797502
A/Accession: B57511
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-418 <MND>
A/Cross-references: GB:U28015; NID:g975300; PIDN:AAV5172.1; PID:g903936

R/Fauchou, C.; Blanchet, A.M.; Collard-Ducilleul, V.; Lalanne, J.L.; Du-Hercend, A.
Eur. J. Biochem. 236, 207-213, 1996
A/Title: Identification of a cysteine protease closely related to interleukin-1-beta-c
A/Reference number: S62183; MUID:96184699; PMID:8617266
A/Accession: S62183
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 55-317; V, 319-418 <FAU>
A/Cross-references: EMBL:X54993; NID:g1155085; PIDN:CA64450.1; PID:g1155086
C/Keywords: cysteine proteinase; hydrolase

Query Match 7.7%; Score 138.5; DB 2; Length 418;

Best Local Similarity 23.4%; Pred. No. 0.006;

Matches 77; Conservative 52; Mismatches 125; Indels 75; Gaps 16;

Qy 10 KSDVSSLIPLMKD-----YMGKG---KISKEKSLDLVLELEKUNLVAPQDLLE 57
Db 50 KKTIVKMLEYLGKDVHLGVFNVLAKHDVLTKEEKKKKYDAKIEDKALIV-----DSLRL 104
Qy 58 KCLKNHRIIDLKTKIQKYQSGVQAGTSYRNLQAIQKSLKDPSENNF-----REEPYK 112
Db 105 K-NVAAHQFTQT-LINMDQKI---TSVKPLQIBAGPEPASSTNLKLCPEEEFRL 158
Qy 113 SIOSEAFPLPQSIPEERYKKSKPLGICLI-----DCIGNETELRDT 156
Db 159 CKQNHDEIVYIKKREDRR-----LALICNTKFDHLPARNGAHYDIVG-----MKRL 206
Qy 157 FTSIGYEVQKPLHLSMGISQILGQFACMPPEHRDYSFVCLVSRGSGSYGV---DQT 213
Db 207 LQGLGTVVDEKTLTRDSESVLRPAARPEKSSDSTFLVMSHGLEIGCTRAHKKK 266
Qy 214 HSGLPPLHIRMFKMGDCSPYLAGKPKMFTIQYVSDQ-----LEDS--SLLSEVDGPA 265
Db 267 PDVLVDITFQIRNNNCISLMDKPVLIYQ---ACREKKGELVWRSPASLAVISGS 323
Qy 266 MKQVFPQKRGCLTVHREADPFMSLCTA 294
Db 324 SENLEADS---VCKIHEKDFI-AFCSS 347

RESULT 11

A56084
Interleukin-1beta converting enzyme beta isoform - human

C/Species: Homo sapiens (man)

C/Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999

C/Accession: A56084

R/Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.

J. Biol. Chem. 270, 4312-4317, 1995

A/Title: Cloning and expression of four novel isoforms of human interleukin-1beta conv

A/Reference number: A56084; MUID:95181414; PMID:7876192

A/Accession: A56084

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-383 <ALN>

A/Cross-references: GB:U13697; NID:g717039; PIDN:AAC50107.1; PID:g717040

C/Genetics:

A/Gene: IL1BC3

C/Keywords: alternative splicing

Query Match 7.6%; Score 136; DB 2; Length 383;

Best Local Similarity 24.0%; Pred. No. 0.0033;

Matches 61; Conservative 54; Mismatches 145; Indels 58; Gaps 12;

Qy 24 MGRGKTSKEKSLDLVLELEKUNLVAPQDLLEKLNHRIIDLKTKIQKYQSGV--- 80
Db 17 MGRGGIN---GLIDELQITRVLNKEMKEVKNENATVMDKRALIDSVIFGAQACQICI 73
Qy 81 -----GAGTSYRNLQAIQKSLKDPSENNFEEPYK-SIOSEAFPLPQSIPEERY 130
Db 74 TYICEDSYLAGTIGLSAPQAVQDNPMAPFTSSGSEGVKLCSLPEAGRIKKQSAETYP 133
Qy 131 KM-XSRPLQICLI-----DCT---GNTELLRDT--FTSIGYEVQKPLHLSMGISQI 178

Db 134 IMKSSRTPLALLICNEEFSDIPRTGAEDVITGMTLMLONTGYSDVYKKNLTASDMTE 193
 Cy 179 LGFACMCEHRDSDSPFCVLYSRGSGSYVG--VQOTSGCLPLHIRMFMGDSCEPLA 235
 Db 194 LEAFAPHEKHTDSTFLVFMSSHGIREGICGKKHSEQVPDIILQALAFMMLNTKNCPSLK 253
 Cy 236 GKPMPEFIQ-----NYVVSQGLEDSLLLEVDPAMKNVBEKAKRGICLCTVA 282
 Db 254 DKPVLITLQACRGDSPGVWFVKDSVGSNLSLPTTEEFEDAIKK-----AH 301
 Cy 263 READPFWSLCTADMSLLEQSH--SSPLYLQCLSQKLRQ 319
 Db 302 IENKDFI-AFCSSTPDNVSRHPTMGVFIQRLIEHMOE 338

RESULT 12

JC7123

Caspase-9 long chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001

C:Accession: JC7123

R:Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.

Biochem. Biophys. Res. Commun. 264, 550-555, 1999

A:Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9

A:Reference number: JC7123; MUID:20001956; PMID:10529400

A:Accession: JC7123

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-454 <FUJ>

A:Cross-references: DDBJ:AB019600; NID:G6440941; PID:G6440942

Query Match 7.4%; Score 134; DB 2; Length 454;

Best Local Similarity 33.1%; Pred. No. 0.015; Matches 45; Conservative 15; Mismatches 52; Indels 24; Gaps 6;

Cy 130 YKMSKPLGICLIID-----IGNET-----ELRLDTFTSLGYEQKFLHSMGI 175
 Db 191 YTLDSDCGHCILINNNPFRSSGSLGTRGCSNIDRKLHRRMLRFMVEVNDLTAKM 250
 Cy 176 SQTIGFACMCEHRDSDSPFCVLYSRGSGS-----YGVQDQHSGLPLHIRMFMG 228
 Db 251 VTALMENA-HRNHRALDCFVVVILSHGQASHLQFPGAVYGTD--GGSYSIEKIYINFG 307

Cy 229 DSCPYLAGKPMPEFIQ 244
 Db 308 SGCPSLGKPKLFFIQ 323

RESULT 13

T20038
hypotheoretical protein CaRD1.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T20038

R:Burton, J.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19214

A:Accession: T20038

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-495 <WIL>

A:Cross-references: EMBL:Z81049; PIDN:CA802848.1; GSPDB:GN00022; CESP:CA8D1.2

A:Experimental source: clone CA8D1

C:Genetics:

A:Gene: CESP:CA8D1.2

A:Map position: 4

A:Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 7.2%; Score 129.5; DB 2; Length 495;

Best Local Similarity 24.0%; Pred. No. 0.037;

Matches 63; Conservative 37; Mismatches 86; Indels 77; Gaps 12;

Cy 70 TKIOXKQSVQAGSTRNVLOAIIQKS-----LKDPNNRPREP----- 109

Db 125 TRYHRDVSVSSEFTYQDIYGRARSRSRALHSSDRHNSSPFVNAFPQSPSSANSF 184
 Cy 110 -----VKKSIQSEAPLPQSIPEE-----RYKMSKPLGIC 140
 Db 185 TGCSSLIGYSSRRRSRSKASGPTQYIFHEEDNPFVADPTISRVEDEKTYNRFSSPRGWC 244
 Cy 141 LIID-----CIGNTELLRDTFTSL-----GYEQKFLHSMHGISQILQGFACMPEHR 189
 Db 245 LINNHFEQMPFRNCTKADKDNLTNLPFCMGVTVICKDNLTGRGMLTIRDF--KHE 301
 Cy 190 DY-DSPVCLVSRGSGSYGVQDQHSGLPL--HHIRKFMDSCEPYLAGKPMFIQNY 246
 Db 302 SHGDSAILVILSHGENVILIGVD-----IPSTHEIYDLNNAAPRLANKRIVFVQ-- 355
 Cy 247 VVSDQGLEDS--LLEVDP-PA 265
 Db 356 -ACRGERRDNGFPVLDSVDGVA 377

RESULT 14

A49429

interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000

C:Accession: A49429; T37312

R:Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.W.; Horvitz, H.R.

Cell 75, 641-652, 1993

A:Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian int

A:Reference number: A49429; MUID:94061982; PMID:8242740

A:Accession: A49429

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-503 <YUA>

A:Cross-references: GB:L29052; NID:G650323; PIDN:AAA27982.2; PID:G6503233

A:Note: sequence extracted from NCBI backbone (NCBIN:139825, NCBI:P:139826)

A:Accession: T37312

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-417; R:419-503 <YU2>

A:Cross-references: EMBL:L29052; PIDN:AAA27982.1

C:Genetics:

A:Gene: ced-3

A:Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 463/3

Query Match 7.2%; Score 129.5; DB 2; Length 503;

Best Local Similarity 24.0%; Pred. No. 0.038; Matches 63; Conservative 37; Mismatches 86; Indels 77; Gaps 12;

Cy 70 TKIOXKQSVQAGSTRNVLOAIIQKS-----LKDPNNRPREP----- 109
 Db 126 TRYHRDVSVSSEFTYQDIYGRARSRSRALHSSDRHNSSPFVNAFPQSPSSANSF 185
 Cy 110 -----VKKSIQSEAPLPQSIPEE-----RYKMSKPLGIC 140
 Db 186 TGCSSLIGYSSRRRSRSKASGPTQYIFHEEDNPFVADPTISRVEDEKTYNRFSSPRGWC 245

Cy 141 LIID-----CIGNTELLRDTFTSL-----GYEQKFLHSMHGISQILQGFACMPEHR 189
 Db 246 LINNHFEQMPFRNCTKADKDNLTNLPFCMGVTVICKDNLTGRGMLTIRDF--KHE 302
 Cy 190 DY-DSPVCLVSRGSGSYGVQDQHSGLPL--HHIRKFMDSCEPYLAGKPMFIQNY 246
 Db 303 SHGDSAILVILSHGENVILIGVD-----IPSTHEIYDLNNAAPRLANKRIVFVQ-- 356

Cy 247 VVSDQGLEDS--LLEVDP-PA 265
 Db 357 -ACRGERRDNGFPVLDSVDGVA 378

RESULT 15
 A42677
 interleukin-1 beta converting enzyme (EC 3.4.22.-) - human

C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999

C:Accession: A54263; A42677; S21734; S24164

R:Corretil, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; M
Genomics 20, 468-473, 1994

A:Title: Molecular characterization of the gene for human interleukin-1beta converting e
A:Reference number: A54263; MUID:94307734; PMID:8034320

A:Accession: A54263

A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA

A:Residues: 1-404 <CE2>

A:Cross-references: GR:I27475

R:Corretil, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T.A
Science 256, 97-100, 1992

A:Title: Molecular cloning of the interleukin-1beta converting enzyme.

A:Reference number: A42677; MUID:92229430; PMID:1373520

A:Accession: A42677

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-404 <CER>

A:Cross-references: GB:M81507; NID:G435598; PIDN:AAA66942.1; PID:G186286
R:Thornberry, N.A.; Bull, H.G.; Calalay, J.R.; Chapman, K.T.; Howard, A.D.; Kostura, M.
J.; Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Lamjco, G.; Palyha, O.C.; Raju, S.M.; Ro
cci, M.J.

A:Title: A novel heterodimeric cysteine protease is required for interleukin-1beta proc
A:Reference number: S21734; MUID:92244338; PMID:1574116

A:Accession: S21734

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-404 <THO>

A:Cross-references: EMBL:X65019; NID:G33792; PIDN:CAA46153.1; PID:G33793

Arch. Biochem. Biophys. 296, 698-703, 1992

A:Title: Purification of interleukin-1beta converting enzyme, the protease that cleaves
A:Reference number: S24164; MUID:92337439; PMID:1321594

A:Accession: S24164

A:Status: preliminary

A:Molecule type: protein

A:Residues: 120-135, 'AX', 138-139, 'X', 141-142 <KRO>

C:Genetics:

A:Gene: GDB:111ABC

A:Cross-references: GDB:132368; OMIM:147678

A:Map position: 11q23-11q23

C:Keywords: cysteine proteinase; hydrolase

Query Match 7.0%; Score 126.5; DB 2; Length 404;

Best Local Similarity 23.1%; Pred. No. 0.048; Indels 79; Gaps 14;

Matches 83; Conservative 56; Mismatches 141; Indels 79; Gaps 14;

24 MORGISKEKSFLLVLEKLNLPADDLLEKLNTHRIDLTKIQKYSQVQ--- 80
17 MGEGTIN---GLDLDELQTRVLNKEKEMKVENATVMDKTRALIDSVIPKQAQICICI 73
81 -----GAGT-----SYRVLQA-----AIQKSLKDPNNFREBPV 110
74 TYICEDSYLAGTGLSADQTSQNYLNMQDSQVLSFPAPQAVQDNPAWPTSSGSEGNV 133
111 KK-STQSESAFIPQSIPEERYKM-KSKPLGICLIT---DCI---GNETELLRDT--F 157
134 KLCSTLEAQRITMKQSAIYIPIMDKSSRTALILICNEFFDSIPRTGAVIDITGMTMLL 193
158 TSLGTEVOKFLHLSMHGISOILGQFACMPEHRDYDSFVCVLSVRSQSQSYG--VDQTH 214
194 QNLGYSVDVKQLTASDWTLEFAFARPEHKTSDSFTLVFMHGIRREGICGKHSQVVP 253
215 SGLPLHTRRMFMGSCPYLAGKPMFFIQ-----NYVSDQLEDSSLLLEV 261
254 DILQNALFNNLNTKNCSLDKRKRVIIIIQACRGDSPGVVWPKDSVGSNLSLPTTEEF 313
262 DGPANKEVEFKAQKGLCTVHREADFWSLCTADMSLLEQSH-SSPSLYIQCTISQKLRQ 319
314 EDDAIKK-----AHIEKDFI-AFCSSTPDNVSWRHPTMGSVFGRLEHMC 359

Search completed: September 8, 2004, 05:50:30
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:48:38 ; Search time 13 Seconds

(without alignments)
1393.878 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDLPKDVSLIFLM.....ITEXKMHFSSIGLITLDEL 348

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|--------|--------------------|-------|-------------|
| 1 | 1635 | 90.8 | 480 1 | CFLA_HUMAN |
| 2 | 1006.5 | 55.9 | 484 1 | CFLA_MOUSE |
| 3 | 313 | 17.4 | 479 1 | ICB3_HUMAN |
| 4 | 297 | 16.5 | 480 1 | ICB3_MOUSE |
| 5 | 248.5 | 13.8 | 521 1 | ICB3_HUMAN |
| 6 | 199 | 11.1 | 293 1 | ICB3_MOUSE |
| 7 | 195.5 | 10.9 | 424 1 | ICB3_HUMAN |
| 8 | 188.5 | 10.5 | 277 1 | ICB3_MOUSE |
| 9 | 185.5 | 10.3 | 282 1 | ICB3_MOUSE |
| 10 | 183.5 | 10.2 | 277 1 | ICB3_MOUSE |
| 11 | 183.5 | 10.2 | 277 1 | ICB3_MOUSE |
| 12 | 183.5 | 10.2 | 277 1 | ICB3_MOUSE |
| 13 | 179.5 | 10.0 | 435 1 | ICB3_MOUSE |
| 14 | 177.5 | 9.9 | 435 1 | ICB3_MOUSE |
| 15 | 172.5 | 9.6 | 276 1 | ICB3_MOUSE |
| 16 | 167.5 | 9.3 | 303 1 | ICB3_MOUSE |
| 17 | 167.5 | 9.3 | 312 1 | ICB3_MOUSE |
| 18 | 166 | 9.2 | 366 1 | ICB3_MOUSE |
| 19 | 166 | 9.2 | 416 1 | ICB3_MOUSE |
| 20 | 163.5 | 9.1 | 303 1 | ICB3_MOUSE |
| 21 | 162.5 | 9.0 | 303 1 | ICB3_MOUSE |
| 22 | 150 | 8.3 | 323 1 | ICB3_MOUSE |
| 23 | 149.5 | 8.3 | 339 1 | ICB3_MOUSE |
| 24 | 145 | 8.1 | 382 1 | ICB3_MOUSE |
| 25 | 142.5 | 7.9 | 299 1 | ICB3_MOUSE |
| 26 | 138.5 | 7.7 | 418 1 | ICB3_MOUSE |
| 27 | 134.5 | 7.5 | 419 1 | ICB3_MOUSE |
| 28 | 129.5 | 7.2 | 503 1 | ICB3_MOUSE |
| 29 | 127.5 | 7.1 | 404 1 | ICB3_MOUSE |
| 30 | 127.5 | 7.1 | 404 1 | ICB3_MOUSE |
| 31 | 126.5 | 7.0 | 404 1 | ICB3_MOUSE |
| 32 | 125.5 | 7.0 | 373 1 | ICB3_MOUSE |
| 33 | 124.5 | 6.9 | 410 1 | ICB3_MOUSE |

| | | | | | |
|----|-------|-----|--------|------------|--------------------|
| 34 | 122 | 6.8 | 241 1 | CFLA_MOUSE | Q98325 moluscum c |
| 35 | 121.5 | 6.7 | 402 1 | ICB3_MOUSE | P43527 rattus norv |
| 36 | 121 | 6.7 | 377 1 | ICB3_MOUSE | O75601 bos taurus |
| 37 | 119.5 | 6.6 | 404 1 | ICB3_MOUSE | Q9m277 canis fam1 |
| 38 | 117.5 | 6.5 | 496 1 | ICB3_MOUSE | P45436 caenorhabdi |
| 39 | 116 | 6.4 | 377 1 | ICB3_MOUSE | P45662 homo sapien |
| 40 | 109.5 | 6.1 | 402 1 | ICB3_MOUSE | P29452 mus musculu |
| 41 | 99.5 | 5.5 | 510 1 | ICB3_MOUSE | Q98325 yaba-like d |
| 42 | 98.5 | 5.5 | 693 1 | ICB3_MOUSE | Q98325 mycoplasma |
| 43 | 97.5 | 5.4 | 2104 1 | ICB3_MOUSE | Q14157 schizosacch |
| 44 | 96.5 | 5.2 | 1893 1 | ICB3_MOUSE | Q96582 homo sapien |
| 45 | 94.5 | 5.2 | 344 1 | ICB3_MOUSE | P52610 borrelia bu |

ALIGNMENTS

RESULT 1

CFLA_HUMAN STANDARD; PRT; 480 AA.

AC 015519; 014673; 014674; 014675; 015137; 015138; 015356; 015510;
AC 043618; 043619; 043620; 060458; 060459; 095784; 095785;
DT 16-OCT-2001 (Rel. 40) Created
DT 16-OCT-2001 (Rel. 40) Last sequence update
DT 15-MAR-2004 (Rel. 43) Last annotation update
DE CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like
DE inhibitory protein) (c-FLIP) (Caspase-eight-related protein) (Casp8)
DE (Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related
DE inducer of toxicity) (MRT) (Caspase homolog) (CASH) (Inhibitor of
DE FLICE) (F-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1)
DE (Bubrin)
GN CFLAR OR CLARP OR MRT OR CASH.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1, 13 AND 14), AND MUTAGENESIS OF
RP TYR-360.
RC TISSUE=Embryonic kidney, and Umbilical vein endothelial cells;
RX MEHLIN=97352452; PubMed=9208847;
RA Shu H.-B., Halpin D.R., Goeddel D.V.;
RT "Casp8 is a FADD- and caspase-related inducer of apoptosis.";
RL Immunity 6:751-763(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).
RX MEHLIN=97470967; PubMed=9326610;
RA Har D.K.M., Chaudhary P.M., Wright M.E., Friedman C., Trask B.J.,
RA Riedel R.T., Baskin D.G., Schwartz S.M., Hood L.;
RT "MRT, a novel death-effector domain-containing protein, interacts
RT with caspases and BclXL and initiates cell death.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11335-11338(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Peripheral blood lymphocytes;
RX MEHLIN=97360133; PubMed=9217161;
RA Immler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V.,
RA Boehmer U., L., Schreiber M., Burns K., Mattmann C., Rindold D.,
RA French L.E., Tschopp U.;
RT "Inhibition of death receptor signals by cellular FLIP.";
RL Nature 388:190-195(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1, 8; 9 AND 10), AND MUTAGENESIS OF
RP ASP-376.
RC TISSUE=T-cell;
RX MEHLIN=97373543; PubMed=9228018;
RA Srinivasula S.M., Ahmad M., O'Connell S., Bullrich F., Banks S.,
RA Wang Y., Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
RA Armstrong R.C., Alnemri E.S.;
RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT Fas/TNFR1-induced apoptosis.";
RL J. Biol. Chem. 272:18542-18545(1997).
RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Embryonal vein endothelial cells;
 RA MEDLINE=97362203; PubMed=9211860;
 RL Hu S., Vincenz C., Ni J., Gentz R., Dixit V.M.;
 RT "I-FLICE, a novel inhibitor of tumor necrosis factor receptor-1- and
 RT CD-95-induced apoptosis.";
 RL J. Biol. Chem. 272:17255-17257(1997).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 7).
 RL Hu S., Dixit V.M.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 11 AND 12).
 RC TISSUE=Kidney;
 RA MEDLINE=99218584; PubMed=10200473;
 RA Rasper D.M., Vallancourt J.P., Hadano S., Houtzager V.M., Seiden I.,
 RA Keen S.L.C., Tawa P., Xanthoudakis S., Nasir U., Matindale D.,
 RA Koop B.F., Peterson E.P., Thornberry N.A., Huang J., Macpherson D.P.,
 RA Black S.C., Hornung F., Lenardo M.J., Hayden M.R., Roy S.,
 RA Nicholson D.W.;
 RT "Cell death attenuation by 'Usurpin', a mammalian DISC-caspase
 RT homologue that precludes caspase-8 recruitment and activation by the
 RT CD-95 (Fas, APO-1) receptor complex.";
 RL Cell Death Differ. 5:271-288(1998).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Skin fibroblast;
 RA MEDLINE=97426025; PubMed=9289491;
 RA Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
 RA Brodianski V.M., Wallach D.;
 RT "CASH, a novel caspase homologue with death effector domains.";
 RL J. Biol. Chem. 272:19641-19644(1997).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Colon carcinoma;
 RA MEDLINE=98021435; PubMed=9380701;
 RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
 RT "CLARP, a death effector domain-containing protein interacts with
 RT caspase-8 and regulates apoptosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA MEDLINE=21100893; PubMed=11161814;
 RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
 RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
 RA Ikeda J.-E., Hayden M.R.;
 RT "Cloning and characterization of three novel genes, A1S2CR1, A1S2CR2,
 RT and A1S2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
 RT critical region at chromosome 2q33-q34: candidate genes for ALS2.";
 RL Genomics 71:200-213(2001).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lymph;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schlier G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang U., Hsieh P.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stachlehn M.J., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cammici P., Prange C.,
 RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mallory S.U.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]
 RP FUNCTION.
 RA MEDLINE=9909897; PubMed=9889531;
 RA Scalfidi C., Schmitz I., Krammer P.H., Peter M.E.;
 RT "The role of c-FLIP in modulation of CD95-induced apoptosis.";
 RL J. Biol. Chem. 274:1541-1546(1999).
 RN [13]
 RP INDUCTION
 RA MEDLINE=99244884; PubMed=10227994;
 RA Algeciras-Schimnich A., Griffith T.S., Lynch D.H., Pava C.V.;
 RT "Cell cycle-dependent regulation of FLIP levels and susceptibility to
 RT Fas-mediated apoptosis.";
 RL J. Immunol. 162:5205-5211(1999).
 CC -1- FUNCTION: Apoptosis regulator protein which may function as a
 CC crucial link between cell survival and cell death pathways in
 CC mammalian cells. Acts as an inhibitor of TNFRSF6 mediated
 CC apoptosis. A proteolytic fragment (p43) is likely retained in the
 CC death-inducing signaling complex (DISC) thereby blocking further
 CC recruitment and processing of caspase-8 at the complex. Full
 CC length and shorter isoforms have been shown either to induce
 CC apoptosis or to reduce TNFRSF6-triggered apoptosis. Lacks enzymatic
 CC (caspase) activity.
 CC -1- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-
 CC inducing signaling complex (DISC) formed by TNFRSF6, FADD and
 CC caspase-8. A proteolytic fragment (p43) stays associated with the
 CC DISC. Also interacts with caspase-10, caspase-3, TRAF1, TRAF2 and
 CC Bcl-X(L) (in vitro).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=14;
 CC Name=1; Synonyms=FLIP-L, CLARP1, MTR1 alpha-1, CASH alpha, I-FLICE
 CC Name=2; Synonyms=FLIP-S, CLARP2, MTR1 beta-1, CASH beta;
 CC Name=3; Synonyms=FLIP-2; Sequence=VSP_000828; VSP_000829;
 CC Name=4; Synonyms=FLIP-3; Sequence=VSP_000824; VSP_000838;
 CC Name=5; Synonyms=FLIP-4; Sequence=VSP_000825;
 CC Name=6; Synonyms=FLIP-5; Sequence=VSP_000840;
 CC Name=7; Synonyms=FLIP-6; Sequence=VSP_000826; VSP_000841;
 CC Name=8; Synonyms=FLIP-7; Sequence=VSP_000824; VSP_000827; VSP_000838;
 CC Name=9; Synonyms=FLIP-8; Sequence=VSP_000830;
 CC Name=10; Synonyms=FLIP-9; Sequence=VSP_000830; VSP_000836; VSP_000837;
 CC Name=11; Synonyms=FLIP-10; Sequence=VSP_000834; VSP_000835;
 CC Name=12; Synonyms=FLIP-11; Sequence=VSP_000838;
 CC Name=13; Synonyms=FLIP-12; Sequence=VSP_000832; VSP_000833;
 CC Name=14; Synonyms=FLIP-13; Sequence=VSP_000831;
 CC Name=15; Synonyms=FLIP-14; Sequence=VSP_000839;
 CC -1- TISSUE SPECIFICITY: Widely expressed. Higher expression in
 CC skeletal muscle, pancreas, heart, kidney, placenta, and peripheral
 CC blood leukocytes. Also detected in diverse cell lines. Isoform 8
 CC is predominantly expressed in testis and skeletal muscle.
 CC -1- INDUCTION: Repressed by IL-2 after TCR stimulation, during
 CC progression to the S-phase of the cell cycle.
 CC -1- DOMAIN: The caspase domain lacks the active sites residues
 CC involved in catalysis.
 CC -1- PTM: Proteolytically processed; probably by caspase-8. Processing
 CC likely occurs at the DISC, generates subunit p43 and p12.
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 2 death effector (DED) domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

Query Match 90.8%; Score 1635; DB 1; Length 480;
 Best Local Similarity 94.1%; Pred. No. 1e-114;
 Matches 319; Conservative 2; Mismatches 0; Indels 16; Gaps 1;

QY 1 MAEIGEDLDSDVSLIFLMKDMYMGKISKESKSPFLDVLVELEKNTLVAPODLLEKCL 60
 DB 97 MAEIGEDLDSDVSLIFLMKDMYMGKISKESKSPFLDVLVELEKNTLVAPODLLEKCL 156
 QY 61 KNHRIIDLKRIKRYKQSVQAGTSRYNVLQALQKSLDPPNNRNLHNGSKREQLKEQ 106
 DB 157 KNHRIIDLKRIKRYKQSVQAGTSRYNVLQALQKSLDPPNNRNLHNGSKREQLKEQ 216
 QY 107 ---EEPVKKSIOESBAFLPQSIPEERYKMKSPKPGICILIDICINTELLRLDTFTSLGY 162
 DB 217 LGAQOEPEVKKSIOESBAFLPQSIPEERYKMKSPKPGICILIDICINTELLRLDTFTSLGY 276
 QY 163 EYQKFLHLSHNGISQILGQAPCMPEHRDVPFCVYVSGSGSOSVYGDOCHSGPLHNI 222
 DB 277 EYQKFLHLSHNGISQILGQAPCMPEHRDVPFCVYVSGSGSOSVYGDOCHSGPLHNI 336
 QY 223 RRMFGDSCFYLAGKPMFPIQNYVYVSDQLEDSSLEVDGPMKNVFEKQKRGCLTVH 282
 DB 337 RRMFGDSCFYLAGKPMFPIQNYVYVSEGLDSSLEVDGPMKNVFEKQKRGCLTVH 396
 QY 283 READFMWLTCTADMSLLEQSHSPSLYICLSKLRQER 321
 DB 397 READFMWLTCTADMSLLEQSHSPSLYICLSKLRQER 435

RESULT 2
 CELA_MOUSE STANDARD; PRT; 484 AA.

AC 035732; 035707; 035733;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE CASP8 and PADD-like apoptosis regulator precursor (Cellular FLICE-like
 DE inhibitor protein) (c-FLIP) (Caspase-eight-related protein) (Casper)
 DE (Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related
 DE inducer of toxicity) (WRT) (Caspase homolog) (CASH) (Inhibitor of
 DE FLICE) (1-FLICE) (PADD-like antiapoptotic molecule 1) (Flame-1)
 DE (Ueaurin).
 CC CFLAR OR CASH.
 CC Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC [1]
 CC SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 CC TISSUE=Liver;
 CC MEDLINE=97426025; PubMed=9289491;
 RA Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
 RA Brodianskii V.M., Wallach D.;
 RA "CASH, a novel caspase homologue with death effector domains.";
 RT J. Biol. Chem. 272:19641-19644(1997).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RN TISSUE=Heart;
 RN MEDLINE=97360133; PubMed=9217161;
 RA Imbler W., Thome W., Hanne W., Schneider P., Hofmann K., Steiner V.,
 RA Boemer J.-L., Schrieter M., Burris K., Mattemann C., Rimoldi D.,
 RA French L.E., Tschoep J.;
 RT "Inhibition of death receptor signals by cellular FLIP.";
 RT Nature 388:190-195(1997).
 RN [3]
 RN FUNCTION.
 RN MEDLINE=20350661; PubMed=10894163;
 RA Yeh W.-C., Irie A., Elia A.J., Ng M., Shu H.-B., Wakeham A.,
 RA Mitsos C., Suzuki N., Bonnard M., Goeddel D.V., Mak T.W.,
 RT "Requirement for Casper (c-FLIP) in regulation of death
 RT receptor-induced apoptosis and embryonic development.";
 RT Immunity 12:633-642(2000).

RN [4]
 RP FUNCTION.
 RX MEDLINE=20069388; PubMed=10602037;
 RA Wang J., Lobito A.A., Shen F., Hornung F., Winoto A., Ienardo M.J.;
 RT "Inhibition of Fas-mediated apoptosis by the B cell antigen receptor
 RT through c-FLIP.";
 RT Eur. J. Immunol. 30:155-163(2000).
 CC -1- FUNCTION: Apoptosis regulator protein which may function as a
 CC crucial link between cell survival and cell death pathways in
 CC mammalian cells. Acts as an inhibitor of TNFRSF6 mediated
 CC apoptosis. A proteolytic fragment (p43) is likely retained in the
 CC death-inducing signaling complex (DISC) thereby blocking further
 CC recruitment and processing of caspase-8 at the complex. Full
 CC length and shorter isoforms have been shown either to induce
 CC (caspase) activity (By similarity).
 CC -1- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-
 CC inducing signaling complex (DISC) formed by TNFRSF6, FADD and
 CC caspase-8. A proteolytic fragment (p43) stays associated with the
 CC DISC (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=FLIP-L, CASH alpha;
 CC IsoId=O35732-1; Sequence=Displayed;
 CC Name=2; Synonyms=FLIP-S, CASH beta;
 CC IsoId=O35732-2; Sequence=VSP_000842, VSP_000843;
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart.
 CC -1- DEVELOPMENTAL STAGE: At embryonic days E9.5 and E10.5 highest
 CC expression in developing heart.
 CC -1- INDUCTION: Isoform 1 but not isoform 2 is activated by BCR cross-
 CC linking in primary B-cells.
 CC -1- DOMAIN: The caspase domain lacks the active sites residues
 CC involved in catalysis.
 CC -1- PTM: Proteolytically processed, probably by caspase-8. Processing
 CC likely occurs at the DISC, generates subunit p43 and p12 (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 2 death effector (DED) domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y14041; CAA74368.1; -;
 DR EMBL; Y14042; CAA74369.1; -;
 DR EMBL; U97076; AAC53281.1; -;
 DR HSSP; O15806; ICDU.
 DR MEROPS; C14.974; -;
 DR MGD; MGT1336166; Cflar.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR001309; ICB_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF01335; DED; 2.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR SMART; SM00031; DED; 2.
 DR SMART; SM00015; CASC; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS50168; DED; 2.
 KW Apoptosis; Repeat; Alternative splicing.
 FT CHAIN 1 380
 FT CHAIN 381 484
 FT CHAIN 485 484
 FT DOMAIN 6 78
 FT DOMAIN 97 175
 FT DOMAIN 268 363
 FT DOMAIN 421 425
 FT VARSPIC 208 218
 FT 21.

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FT  VARSLIC      219      480      /Ffid=VSP_000642.
FT  MISSING (In Isoform 2).
FT  FTID=VSP_000643.
FT  CONFLICT     123      125      MISSING (IN REF. 2).
SQ  SEQUENCE     484 AA, 55245 MW, 08F7A92CB095F1F CRC64;

Query Match      55.9%; Score 1006.5; DB 1; Length 484;
Best Local Similarity 62.1%; Pred. No. 8.5e-68;
Matches 211; Conservative 41; Mismatches 67; Indels 21; Gaps 6;

QY  1 MAEIGEDJDKSPVSSFLFL---MMDYGRGKISKSEKSFLLVYVELEKLNIVAPDQDLE 57
D  102 LWEIGESLDQNDVSSLVFLTRITRDYGRKINAKDSFLLVLEKLNIVASDQNLLE 161
QY  56 KCLKNIRIDLEKTKIQYKQSGVQAGTSYRNVLQALQK-SLADPS---NNFREEP----- 109
D  162 KCLKNIRIDLEKTKIQYKQSGVQAGTSYRNVLQALQK-SLADPS---NNFREEP----- 109
QY  110 -----VKRSIQSEAFPLQSPPEERYKMKSPLEICILIDICIGETELLADFTSTIG 161
D  221 YRDSQRTLVKTSIQSGAFPLPHIREETRYKQSPKPDICILIDICIGETELLADFTSTIG 280
QY  162 YEVOKFLHLSMHGISQLIGFACPMPEHRDYSFVCVIVSRGSGSYGVVDQTSGLPLH 221
D  281 YHIOQLFPPKHHDITQIVRYASMAQODYDSFACVIVSISGSGSMWGRQVHSGFSLH 340
QY  222 IRRMFGDCPYLAGKPKMFTIONVYVSDGLEDSLLEVDGPMKNVEFKAGKGLCTV 281
D  341 YKMFPTGTCTSLRKPPLFPIQVYESIGSQLEBSS-LEVDGSGIKKVDSPKLPQPHCTT 399
QY  282 HREADFPMWLCCTADWMLLEQSHSPSYLQCLISQXKRCR 321
D  400 HREADFPMWLCCTADWMLLEQSHSPSYLQCLISQXKRCR 439

DB  400 HREADFPMWLCCTADWMLLEQSHSPSYLQCLISQXKRCR 439

RESULT 3
ICB8 HUMAN      STANDARD:      PR1, 479 AA.
ID  ICB8 HUMAN      STANDARD:      PR1, 479 AA.
AC  Q14750; Q14676; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796;
AC  Q15780; Q15805; Q8TD11; Q8TD12; Q8TD13; Q8TD14; Q8TD15; Q8TD15; Q8TD15;
AC  Q9COK4; Q9COK1;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)
DE  (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
DE  like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)
DE  (Apoptotic protease Mch-5) (CAP4).
GN  CASP8 OR MCH5.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_Taxid=9606;
RN  [1]
RN  SEQUENCE FROM N.A. (ISOFORMS 1, 2, 3, 5, 6, 7 AND 8).
RC  TISSUE=B-cell, and Thymus;
RX  MEDLINE=96279827; PubMed=8681376;
RX  BOLDIN M.P., Goncharov T.M., Golisev Y.V., Wallach D.;
RT  "Involvement of MACH, a novel MORT1/FADD-interacting protease, in
RT  Fas/Apo-1 and TNF receptor-induced cell death.";
RL  Cell 85:817-827(1996).
RN  [2]
RN  SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RX  MEDLINE=96279827; PubMed=8681377;
RX  Muzio M., Chinaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
RX  Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
RX  Kramer P.H., Peter M.E., Dixit V.M.;
RT  "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
RT  to the CD95 (Fas/Apo-1) death-inducing signaling complex.";
RL  Cell 85:817-827(1996).
RN  [3]
RN  SEQUENCE FROM N.A. (ISOFORM 4).
RN  TISSUE=T-cell;
RX  MEDLINE=96351838; PubMed=8755496;
RX  Fernandes-Alnemri T., Armstrong R.C., Krebs J.F., Srinivasula S.M.,
RX  Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RX  Litwack G., Alnemri E.S.;
RT  "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT  apoptotic cysteine protease containing two FADD-like domains.";
RT  Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN  [4]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=99132295; PubMed=9931493;
RX  Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
RT  "Structure and chromosome localization of the human Casp8 gene.";
RL  Gene 226:225-232(1999).
RN  [5]
RN  SEQUENCE FROM N.A. (ISOFORM 2).
RX  MEDLINE=97373543; PubMed=9228018;
RX  Srinivasula S.M., Ahmad M., O'Callaghan S., Bullrich F., Banks S.,
RX  Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
RX  Armstrong R.C., Alnemri E.S.;
RT  "FAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT  Fas/TNFR1-induced apoptosis.";
RL  J. Biol. Chem. 272:18542-18545(1997).
RN  [6]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=21100893; PubMed=11161814;
RX  Hadano S., Yanagisawa Y., Skaug J., Richter K., Nasir J.,
RX  Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RX  Ikeda J.-E., Hayden M.R.;
RT  "Cloning and characterization of three novel genes, A152CR1, A152CR2,
RT  and A152CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT  critical region at chromosome 2q33-q34: candidate genes for ALS2.";
RL  Genomics 71:200-213(2001).
RN  [7]
RN  SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.
RC  TISSUE=Leukocyte;
RX  MEDLINE=22005982; PubMed=12010809;
RX  Himeji D., Horikuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
RX  Harada M.;
RT  "Characterization of caspase-8L, a novel isoform of caspase-8 that
RT  behaves as an inhibitor of the caspase cascade.";
RL  Blood 99:4070-4078(2002).
RN  [8]
RN  SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 9), AND INTERACTION OF ISOFORM 9
RN  WITH BAP31 AT THE ENDOPLASMIC RETICULUM.
RX  MEDLINE=21927603; PubMed=11917123;
RX  Breckenridge D.G., Nguyen M., Kuprij S., Reith M., Shore G.C.;
RT  "The procaspase-8 isoform, procaspase-8L, recruited to the BAP31
RT  complex at the endoplasmic reticulum.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).
RN  [9]
RN  SEQUENCE FROM N.A. (ISOFORM 7).
RC  TISSUE=Leukocyte;
RX  MEDLINE=22388257; PubMed=12477932;
RX  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX  Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RX  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RX  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hultx R.A.,
RX  Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX  Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
RX  Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RX  Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RX  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RX  Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hultx R.A.,
RX  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RX  Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RX  Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RX  Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RX  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RX  Butcherfield Y.S.N., Krzyzanski M.I., Skalska U., Smailus D.E.,
RX  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length
RT  human and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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[10] PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE=97121412; PubMed=8962078;
RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.,
RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
CD95-like cysteine proteases.",
Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
[11] FUNCTION.
RX MEDLINE=97160607; PubMed=9006941;
RA Muzio M., Salvesen G.S., Dixit V.M.;
RT "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
zymogens.",
J. Biol. Chem. 272:29562-2956(1997).
[12] PROCESSING.
RX MEDLINE=97337557; PubMed=9184224;
RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
RA Kramer P.H., Peter M.E.;
RT "FLICE is activated by association with the CD95 death-inducing
signaling complex (DISC).",
EMBO J. 16:2794-2804(1997).
[13] CHARACTERIZATION OF ISOFORM 7.
RX MEDLINE=20318377; PubMed=10960845;
RA Horikuchi T., Himeji D., Tsukamoto H., Haraishi S., Hashimura C.,
RA Hayashi K.;
RT "Dominant expression of a novel splice variant of caspase-8 in human
peripheral blood lymphocytes.",
Biochem. Biophys. Res. Commun. 272:877-881(2000).
[14] INTERACTION WITH BCL2; BCL2L1 AND BCL2L1.
RX MEDLINE=97477382; PubMed=9334338;
RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
RA Cromlish J.A., Shore G.C.;
RT "p28 Bap1, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
endoplasmic reticulum.",
J. Cell Biol. 139:327-338(1997).
[15] INTERACTION WITH PEA15.
RX MEDLINE=99369240; PubMed=10442631;
RA Condorelli G., Vignolotto G., Cafieri A., Tencina A., Andalo P.,
RA Oriente F., Miele C., Caruso M., Formisano P., Beguinot F.;
RT "PED/PEA-15, an anti-apoptotic molecule that regulates Fas/TNFR1-
induced apoptosis.",
Oncogene 18:4409-4415(1999).
[16] X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=99451259; PubMed=10508784;
RA Blanchard H., Kodandapani L., Mitel P.R.E., Di Marco S., Krebs J.F.,
RA Wu J.C., Tomaselli K.J., Grotter M.G.;
RT "The three-dimensional structural structure of caspase-8: an initiator enzyme in
apoptosis.",
Structure 7:1125-1133(1999).
[17] VARIANT CASP8D TRP-248.
RX MEDLINE=2239940; PubMed=12353635;
RA Chan H.Y., Zheng L., Ahmad M., Wang J., Speirs C.K., Siegel R.M.,
RA Dale J.K., Puck J., Davis J., Hall C.G., Skoda-Smith S.,
RA Atkinson T.P., Straus S.E., Lenardo M.J.;
RT "Allelotropic defects in lymphocyte activation caused by caspase-8
mutations lead to human immunodeficiency.",
Nature 419:395-399(2002).
[18] -1- FUNCTION: Most upstream protease of the activation cascade of
caspases responsible for the TNFRSF6/Fas mediated and TNFRSF1A
induced cell death. Binding to the adapter molecule FADD recruits
it to either receptor. The resulting aggregate called death-
inducing signaling complex (DISC) performs CAS8 proteolytic
activation. The active dimeric enzyme is then liberated from the
DISC and free to activate downstream apoptotic proteases.
Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CAP4, CAP5, CAP6, CAP7, CAP8, CAP9, CAP10, CAP11, CAP12, CAP13,
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CAP424, CAP425, CAP426, CAP427, CAP428, CAP429, CAP430, CAP431,
CAP432, CAP433, CAP434, CAP435, CAP436, CAP437, CAP438, CAP439,
CAP440, CAP441, CAP442, CAP443, CAP444, CAP445, CAP446, CAP447,
CAP448, CAP449, CAP450, CAP451, CAP452, CAP453, CAP454, CAP455,
CAP456, CAP457, CAP458, CAP459, CAP460, CAP461, CAP462, CAP463,
CAP464, CAP465, CAP466, CAP467, CAP468, CAP469, CAP470, CAP471,
CAP472, CAP473, CAP474, CAP475, CAP476, CAP477, CAP478, CAP479,
CAP480, CAP481, CAP482, CAP483, CAP484, CAP485, CAP486, CAP487,
CAP488, CAP489, CAP490, CAP491, CAP492, CAP493, CAP494, CAP495,
CAP496, CAP497, CAP498, CAP499, CAP500, CAP501, CAP502, CAP503,
CAP504, CAP505, CAP506, CAP507, CAP508, CAP509, CAP510, CAP511,
CAP512, CAP513, CAP514, CAP515, CAP516, CAP517, CAP518, CAP519,
CAP520, CAP521, CAP522, CAP523, CAP524, CAP525, CAP526, CAP527,
CAP528, CAP529, CAP530, CAP531, CAP532, CAP533, CAP534, CAP535,
CAP536, CAP537, CAP538, CAP539, CAP540, CAP541, CAP542, CAP543,
CAP544, CAP545, CAP546, CAP547, CAP548, CAP549, CAP550, CAP551,
CAP552, CAP553, CAP554, CAP555, CAP556, CAP557, CAP558, CAP559,
CAP560

CC CASP9 and CASP6 are likely retained in the DISC. Cleaves and
 CC activates CASP3, CASP4, CASP8, CASP7, and CASP10. May
 CC participate in the G2M6 apoptotic pathways. Cleaves ADAPT.
 CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-L-AMC.
 CC Likely target for the cowpox virus CPNA death inhibitory protease.
 CC Isoforms 5, 6, 7 and 8 lack the catalytic site and may interfere
 CC with the pro-apoptotic activity of the complex.
 CC
 CC -1- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
 CC Interacts with FADD, CFLAR and PEAL5. Isoform 9 interacts at the
 CC endoplasmic reticulum with a complex containing BAP1, BAP2,
 CC BCL2L1 and/or BCL2L1.
 CC -1- SUBCELLULAR LOCATION: Cytoplasm;c.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=9;
 CC Name=1; Synonyms=Alpha-1;
 CC IsoId=Q14790-1; Sequence=Displayed;
 CC Name=2; Synonyms=Alpha-2, MCHS-beta;
 CC IsoId=Q14790-2; Sequence=VSP_000810;

Query Match 17.4%; Score 113; DB 1; Length 479;
 Best Local Similarity 26.8%; Pred. No. 5e-16;
 Matches 95; Conservative 75; Mismatches 117; Indels 68; Gaps 14

QY 3 EIGEDLDKSDVSLFLFMKDYGSGIKSKESPLDVLVELEKLNLVAPQDLIEKLCN 62
 Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|
 QY 107 QRSEVSSESRSEPRFLLGEEISKCKDDDMNLDFIEMKEVILGEGLDKLKVCQA 166
 Db ::|||::|||::|||::|||::|||::|||::|||::|||
 QY 63 IHRIDLRKKIKKYCA-----SVQGAGTSYRNVLAOLISLSXDSNNPREPVKSIO 115
 Db ::|||::|||::|||::|||::|||::|||::|||::|||
 QY 167 INKSILRK-IINDYEFPSKERSSLESPPDEFSNGEELCGWTTISDP---RE-----Q 215
 Db ::|||::|||::|||::|||::|||::|||::|||::|||
 QY 116 ESERAFLOPSIPBERRYKMKSKPELGICLIIDICG-----NETEL---LR 154
 Db ::|||::|||::|||::|||::|||::|||::|||::|||
 QY 216 DES--QT-L-DKVYQMSKRGRGCIIINHNHFAKAEREVPKLHSIRDRNGHTLDGAALT 271
 Db ::|||::|||::|||::|||::|||::|||::|||::|||
 QY 155 DPTFTSLGVQVKFKHLNSHGSIQLGGPACMPERRDVSYCVLYVERGSQSIVGYVDTH 214
 Db 272 TTFBELHEIFKHPCDCIVEQVELYLKIYQM-DHSNDCTFCILLHGDKGIITVGDOE 330
 QY 215 SOLPLHHRRRMFGDSPCYLAGKRMFFIQ-----NY-VASGOLEDSSLLEV-DGP 264
 Db :||:|||||::|::|::|::|::|::|::|::|::|::|::|
 QY 331 A-PYEELTSGDTGLKCPSLAKRKVFVIQCAGGDANYOKAPIETDSEEGPYLEMDSLSP 388
 Db :||:|||||::|::|::|::|::|::|::|::|::|::|::|
 QY 265 AKNVEFPAAQRGLCTVIREADPFWSICTADMILLSGHSSPELLYCICSQTKRQ 319
 Db :||:|||||::|::|::|::|::|::|::|::|::|::|::|
 QY 389 QTRYP-----DEADFLLGMATVNMCVSNPAEGTWYTOSLCSQSLRE 431
 Db :||:|||||::|::|::|::|::|::|::|::|::|::|::|

RESULT 4
 ICBS_MOUSE STANDARD; PRT; 480 AA.
 ID AC O89110; O35669;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-8 precursor (EC 3.4.22.-).
 GN CASP8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=129/SvJ;
 RX MEDLINE=9831661; PubMed=9654089;
 RA Sakamaki K., Tsukumo S.-I., Yonehara S.;
 RT "Molecular cloning and characterization of mouse caspase-8.";
 RL Eur. J. Biochem. 253:399-405(1998).
 FN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=99057979; PubMed=9837723;
 RA Van de Craen W., Van Loo G., Declercq W., Schoote P., Fiers W.,
 ZA van den Braken I., Mandruzzato S., van der Bruggen P., Fiers W.

RA Vandenberg P.;
RT "Molecular cloning and identification of murine caspase-8";
RL J. Mol. Biol. 284:1017-1026(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon, and Mammary gland;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Peltingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stadelman M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantucci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusi D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 57-476 FROM N.A.
RA Kioschis P., Kioschik F., Pousatka A., Krammer P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Most upstream protease of the activation cascade of
CC caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
CC induced cell death. Binding to the adaptor molecule FADD recruits
CC it to either receptor. The resulting aggregate called death-
CC inducing signaling complex (DISC) performs CASP8 proteolytic
CC activation. The active dimeric enzyme is then liberated from the
CC DISC and free to activate downstream apoptotic proteases.
CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
CC participate in the G2M6 apoptotic pathways. Cleaves ADPRT.
CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
CC -!- ENZYME REGULATION: Inhibited by Z-VAD-FK, CrmA and P35.
CC -!- SUBUNIT: Heterodimer of a 18 kDa (P18) and a 10 kDa (P10) subunit.
CC -!- INTERACTS WITH FADD, Cflar and Peals (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
CC Highest expression in spleen, thymus, lung, liver and kidney.
CC Lower expression in heart, brain, testis and skeletal muscle.
CC -!- DEVELOPMENTAL STAGE: In the embryo, highest expression occurs at
CC day 7.
CC -!- PTM: Generation of the subunits requires association with the
CC death-inducing signaling complex (DISC), whereas additional
CC processing is likely due to the autocatalytic activity of the
CC activated protease. G2M6 and CASP10 can be involved in these
CC processing events (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 2 death effector (DEE) domains.
CC
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CC
CC EMBL; AF067841; AAC40132.1; -
CC EMBL; AF067835; AAC40132.1; JOINED.
CC EMBL; AF067836; AAC40132.1; JOINED.
CC EMBL; AF067837; AAC40132.1; JOINED.
CC EMBL; AF067838; AAC40132.1; JOINED.

DR EMBL; AF067839; AAC40132.1; JOINED.
DR EMBL; AF067840; AAC40132.1; JOINED.
DR EMBL; AF067834; AAC40131.1; -
DR EMBL; AJ007749; CAA07677.1; -
DR EMBL; BC006737; AAH06737.1; -
DR EMBL; BC049955; AAH49955.1; -
DR EMBL; AJ000641; CAA04196.1; -
DR HSPB; Q15806; ICDU.
DR MEROPS; C14.009; -
DR MGD; MGI:1261423; Casp8.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0005634; Cnucleus; IDA.
DR GO; GO:0004205; F:caspase-8 activity; IDA.
DR GO; GO:0006915; P:apoptosis; IDA.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BENZYM.
DR SMART; SM00115; CASC; 1.
DR SMART; SK00031; DED; 2.
DR PROSITE; PS01124; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50169; DED; 2.
KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Repeat.
FT PROPEP 1 218
FT CHAIN 1 219
FT PROPEP 219 376
FT CHAIN 377 387
FT CHAIN 388 480
FT ACT_SITE 319 319
FT ACT_SITE 362 362
FT DOMAIN 3 80
FT DOMAIN 101 177
FT CONFLICT 68 71
FT CONFLICT 94 99
FT CONFLICT 96 96
FT CONFLICT 103 107
FT CONFLICT 475 475
SQ SEQUENCE 480 AA; 55356 MW; 045268E3DE5ED4F CRC64;
Query Match 16.5%; Score 297; DB 1; Length 480;
Best Local Similarity 26.5%; Pred. No. 7; 9e-15;
Matches 95; Conservative 70; Mismatches 120; Indels 74; Gaps 14;
QY 3 EIGEDDDKSVSLITIMADYMGROGKISKESKSFLLVLEKTLNVAPDQDLEKCKLN 62
DB 107 KLESEVSELEKRFKFLNNELPKCEDDJLLEIFEMERKTLANLETLISICDQ 166
QY 63 IHRIDIKTKIOKY-----KQVOGAGTSYRNVLQAAIQLSK--DPSNNFREPKYS 113
DB 167 VNK-SLLGKIKEDYERSTERMSLEGREBLEPVSVD---EMSLKVAELCDSPRE----- 216
QY 114 IQSEAFPLPOSIDPEERYKXKSLPLGICLI-----DQIGNE 149
DB 217 -QSESRISDQV---YQKNKPRGVCILINNHDFSKAREDTQLRKXKDKRGTDG--D 268
QY 150 TELLRPTSLGVEYKFLHLMHGISQILGQFACMPHPRDYSPFVCLVSRGSGSQSYG 209
DB 269 KEMLSKTFKELHNEIYSYDCTANEHLEBYQ-SADHKKDCICILSHGKGVYGG 327
QY 210 VPDTHGGLPLHITRRFMWDCSPYLAQKPYNFIIQ-----NVV--VSD--GQLEDSLLLE 260
DB 328 TDKKES--IYDLSYFTSKCPSPSLGKXKIFFIACGGSNFQKGVPEADPEEQNNHLE 385
QY 261 VDPGPAKNVPEFKQKGLCTVHREADPFWSLCTAAMSLLEGSHSPSYLTCLCSQKTRQ 319
DB 386 VDSSEKXNY-----IPDEADFLGMAITVKNCSYNRDPVNGVTYIQLSQSLRE 433

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RESULT 5
ICEA_HUMAN          STANDARD;          PRT;          521 AA.
ID AC Q92851; Q8WY08; Q93845; Q9Y2U6; Q9Y2U7;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-10 precursor (EC 3.4.22.-) (ICE-1-like apoptotic protease 4)
DE (Apoptotic protease Mch-4) (PAS-associated death domain protein
DE interleukin-1B-converting enzyme 2) (FLICE2).
DE CASP10 OR MCH4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=T-cell;
RX MEDLINE=9635383; PubMed=8755496;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Litwack G., Alnemri E.S.,
RA "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RA apoptotic cysteine protease containing two FADD-like domains.";
RA Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=9719783; PubMed=9045686;
RA Vincenz C., Dixit V.M.;
RA "Fas-associated death domain protein interleukin-beta-converting
RA enzyme 2 (FLICE2), an ICE/Ced-3 homologue, is proximally involved in
RA CD95- and p55-mediated death signaling.";
RA J. Biol. Chem. 272:6578-6583(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C), AND VARIANT IL6-410.
RC TISSUE=Spleen, and Thymus;
RX MEDLINE=9921459; PubMed=10187817;
RA Ng P.W., Porter A.G., Janicke R.U.;
RA "Molecular cloning and characterization of two novel pro-apoptotic
RA isoforms of caspase-10.";
RA J. Biol. Chem. 274:10301-10308(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=21100893; PubMed=11161814;
RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.;
RA "Cloning and characterization of three novel genes, A1S2CR1, A1S2CR2,
RA and A1S2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RA critical region at chromosome 2q33-q34; candidate genes for ALS2.";
RA Genomics 71:200-213(2001).
RN [5]
RP PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE=97121412; PubMed=8962078;
RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.;
RA "Molecular ordering of the Fas-apoptotic pathway: the Fas/Apo-1
RA protease Mch3 is a CrmA-inhibitable protease that activates multiple
RA Ced-3/ICE-1-like cysteine proteases.";
RA Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
RN [6]
RP VARIANT ALPS2 PHE-285, AND VARIANT IL6-410.
RX MEDLINE=99339325; PubMed=10412980;
RA Wang J., Zheng L., Lobito A., Chan F.K., Dale J., Sneller M., Yao X.,
RA Puck J.M., Straus S.E., Jenaro M.U.;
RA "Inherited human caspase 10 mutations underlie defective lymphocyte
RA and dendritic cell apoptosis in autoimmune lymphoproliferative
RA syndrome type II";
RA Cell 98:47-58(1999).
RN [7]
RP FUNCTION: Involved in the activation cascade of caspases
RN responsible for apoptosis execution. Recruited to both Fas- and
RN TNFR-1 receptors in a FADD dependent manner. May participate in
RN the granzyme B apoptotic pathways. Cleaves and activates caspase-
RN
```

RT family." (1995) .
 RL Cancer Res. 55:2737-2742 (1995) .
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA) .
 RA Kieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Wittek L.A., Nickerson D.A.,
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBD databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA) .
 RC TISSUE=Lung;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Krausner R.D., Collins F.S., Wagner L., Shenon C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat F.,
 RA Hopkins R., Jordan M., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Chappleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussid T.B., Toshimuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting L.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
 RA Schencher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences." .
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .
 RN [4]
 RP PROCESSING.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=97059171; PubMed=8900201;
 RA Strinivasula S.M., Fernandes-Alnemri T., Zangwill J., Robertson N.,
 RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
 RA Alnemri E.S.;
 RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and
 RT the lamin-leaving enzyme Mcclalpha are substrates for the apoptotic
 RT mediator CPP32." .
 RL J. Biol. Chem. 271:27039-27106 (1996) .
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Cleaves poly(ADP-ribose)
 CC polymerase in vitro, as well as lamins. Overexpression promotes
 CC programmed cell death.
 CC -1- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Alpha;
 CC isoIdc=P55212-1; Sequence=Displayed;
 CC Name=Beta;
 CC isoIdc=P55212-2; Sequence=VSP 000805;
 CC -1- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
 CC SUBUNITS
 CC -1- SIMILARITY: Belongs to peptidase family C14.

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 DR EMBL; U20536; AAC50168.1; -
 DR EMBL; U20537; AAC50169.1; -
 DR EMBL; AY254046; AAC63494.1; -
 DR EMBL; BC000305; AAH00305.1; -
 DR EMBL; BC004460; AAH04460.1; -
 DR HSSP; P42574; IPAD.

| | | |
|----|----|---|
| | CC | SRRATN-White leghorn; TISSUE=Covarian granulosa; |
| | RX | MEDLINE=97368127; PubMed=9224894. |
| | RA | Johson A.L., Bridgman J.T., Bergeron L., Yuan J., |
| | RT | "Characterization of the avian Ich-1 cDNA and expression of Ich-1L |
| | RT | mRNA in the hen ovary." |
| | RL | Gene 192:227-233(1997). |
| | CC | -I- FUNCTION: Involved in the activation cascade of caspases |
| | CC | responsible for apoptosis execution. Might function by either |
| | CC | activating some proteins required for cell death or inactivating |
| | CC | proteins necessary for cell survival (By similarity). |
| | CC | -I- ALTERNATIVE PRODUCTS: |
| | CC | Event=Alternative splicing; Named isoforms=2; |
| | CC | Name=ICH-1L; |
| | CC | IsoId=G989943-1; Sequence=Displayed; |
| | CC | Note=Only form found in the ovary; |
| | CC | Name=ICH-IS; |
| | CC | IsoId=G989943-2; Sequence=VSP_000803; VSP_000804; |
| | CC | -I- PTM: Heterodimer of a small and a large subunit (By similarity). |
| | CC | -I- SIMILARITY: Belongs to peptidase family C14. |
| | CC | -I- SIMILARITY: Contains 1 CARD domain. |
| | CC | ----- |
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| | CC | ---- |
| | DR | EMBL: U64963; AAC29881.1; ALT_INIT. |
| | DR | HSSP: P42574; ICP3. |
| | DR | MEROPS; C14.006; ? |
| | DR | InterPro: IPRO01315; CARD. |
| | DR | InterPro: IPR002138; ICE_P10. |
| | DR | InterPro: IPR001309; ICE_P20. |
| | DR | InterPro: IPR002398; Peptidase_C14. |
| | DR | Pfam: PF00619; CARD; 1. |
| | DR | Pfam: Pf00656; Peptidase_C14; 1. |
| | DR | PRINTS: PR00376; ILICENZYM. |
| | DR | SMART: SMO0114; CARD; 1. |
| | DR | SMART: SMO015; CASc; 1. |
| | DR | PROSITE: PS50209; CARD; 1. |
| | DR | PROSITE: PS01122; CASPASS_CYG; 1. |
| | DR | PROSITE: PS01121; CASPASS_HIS; 1. |
| | DR | PROSITE: PS50207; CASPASS_P10; 1. |
| | DR | PROSITE: PS50208; CASPASS_P20; 1. |
| | KW | Hydrolase; Thiol protease; Apoptosis; Zymogen; Alternative splicing. |
| | FT | PROPEP 1 140 |
| | FT | CHAIN 141 308 |
| | FT | CHAIN 309 424 |
| | FT | CHAIN 424 424 |
| | FT | CASPASE-2 SUBUNIT P13 (BY SIMILARITY). |
| | FT | CASPAS-2 SUBUNIT P12 (BY SIMILARITY). |
| | FT | DOMAIN 7 96 |
| | FT | ACT SITE 248 248 |
| | FT | ACT SITE 291 291 |
| | FT | VARSPLIC 1 7 |
| | FT | VARSPLIC 294 424 |
| | SO | SEQUENCE 424 AA; 47959 MW; 7928105f8BBB2F60 CRC64; |
| | | Query Match 10.9%; Score 195.5; DB 1; Length 424; |
| | | Best Local Similarity 22.4%; Pred. No. 2.5e-07; |
| | | Matches 88; Conservative % 62; Mismatches 168; Indels 75; Gaps 12; |
| Oy | : | :MAETIEDDDKSDVSLLFLMKDVGNGGXSKSESLDVVELEKNLVAPQGLDECLC 60 |
| b | : | :::: ::: ::: ::: ::: ::: |
| | : | :28 IKELINHEITDIITTEMVENIOAKSGSSQNVAEPLNLPKR-----GNVAFSAFCAL 81 |

QY 61 KNHRIDTKTKIQKYKQSVGAGTSYRNVLQAAIQSKLPDPSNNFREEPYKSGIOSEAF 120
 Db 82 QETKQCHLAEMILKTNESLSRGDIATLEGRYSNLPPLPSSECSNKRRLIVEHSLSGSDG 141
 QY 121 LPQSTPEER-----YKMKKPLDGLI-----IDCIG 147
 Db 142 PP--TPPVGHCTPEFYRDHQAHLAKLISEPRGLILISNHFSEKOLEYRSGGDVCA- 198
 QY 148 NTELLRDFTSLGYEVOKFLHSMGISQILGQFACMPEHRDVSFVCLVRSQSGQSV 207
 Db 199 -SLELL---FKHLGQVIVFHFDQSAEHESSALHEFSKLPKHODVDSICVALLSHGVEGV 254
 QY 208 YVVDQTHSGPLPHIRRMFMGDSCPYLAGKPKFFIO-----NYVSDGQLEDGS- 257
 Db 255 YGTD--GKLLQLOEAFRLFDNANCPNQNKPFFIOACRQDETDRGVDRDCKERSDSP 312
 QY 258 -LLEVDPGPMKRVFEKQKRG--LC-----TVHRADFEWSLCTADMSLLEGS 302
 Db 313 GGEESDANKENTKRLRLEPESDMTCGACLKGTAAKNTKRGSYITALITVAEDSRDT 372
 QY 303 HSSPSLYLQCLSQKLRQERGTPGSGITSSKDM 335
 Db 373 HVADMLVK--VVRQIKQREGYAPGTEFHRCKEM 403

RESULT 8
 ID ICE3_MOUSE STANDARD; PRT; 277 AA.
 AC P70677; O08668; Q9QW14;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptain precursor (Ec 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
 DE (SCA-1) (LICE).
 GN CASP3 OR CPP32.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G., Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding a cysteine protease resembling interleukin-1 beta converting enzyme and CED-3.";
 RT and CED-3.";
 RT Oncogene 13:749-755(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224429; PubMed=9070890;
 RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
 RT "Specific expression of CPP32 in sensory neurons of mouse embryos and activation of CPP32 in the apoptosis induced by a withdrawal of NGF.";
 RT Biochem. Biophys. Res. Commun. 231:770-774(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361; Declercq W., van den Brande I., van de Craen W., Vandenaebelle P., Schotte P., van Cleefinge W., Beyaert R., Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 RT FEBS Lett. 403:61-69(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Alechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hochline R.F., Jordan H., Moore T., Wax S.T., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywanski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 58-277 FROM N.A.
 RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O., Fortin J.-P., Sekaly R.-P.;
 RT "Multiple pathways of apoptosis converging on the CPP32 protease.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. At the onset of apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase (PAR) at a 216-Asp-1-Gly-217 bond. Cleaves and activatessterol regulatory element binding proteins (SREBPs) between the basic helix-loop-helix leucine zipper domain and the membrane attachment domain. Cleaves and activates caspase-6, -7 and -9 (By similarity).
 CC Cleaves IL-1 beta between an Asp and an Ala, releasing the mature cytokine which is involved in a variety of inflammatory processes.
 CC -1- SUBUNIT: Heterodimer of a 17 Kda (p17) and a 12 Kda (p12) subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highest expression in brain, skeletal muscle and kidney.
 CC -1- TISSUE SPECIFICITY: Highest expression in spleen, lung, liver, kidney and heart. Lower expression in brain, skeletal muscle and testis.
 CC -1- PM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROPEPTASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROPEPTASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
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 CC -----
 DR EMBL; U54803; AAC52768.1; -;
 DR EMBL; U54802; AAC52768.1; JOINED.
 DR EMBL; U49929; AAC52764.1; -;
 DR EMBL; D86352; BAA21727.1; -;
 DR EMBL; Y13086; CAA73528.1; -;
 DR EMBL; U19522; AAC53196.1; -;
 DR EMBL; BC038825; AAH38825.2; -;
 DR EMBL; U63720; AAD09504.1; -;
 DR PIR; JCS410; JCS410.
 DR HSSP; P42574; LPAU.
 DR MEROPS; C14.003; -;
 DR MGDI; MGDI:107739; Casp3.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.

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DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00686; Peptidase_C14; 1.
DR PRINTS: PR00376; ILIBENZYME.
DR SMART: SM00115; CASP; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KM Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT_SITE 121 121
FT ACT_SITE 163 163
FT ACT_SITE 17 17
FT CONFLICT 51 51
FT CONFLICT 63 65
FT CONFLICT 84 84
FT CONFLICT 95 95
FT CONFLICT 97 97
FT CONFLICT 128 128
FT CONFLICT 135 135
FT CONFLICT 231 231
FT CONFLICT 262 262
SQ SEQUENCE 277 AA; 31474 MW; CE91598F74826605 CRC64;

Query Match 10.5%; Score 188.5; DB 1; Length 277;
Best Local Similarity 28.9%; Pred. No. 5e-077; Indels 37; Gaps 11;
Matches 67; Conservative 36; Mismatches 92;

QY 103 NNFEEFV--KKSIOSEAFLPQSIIEERYKMKSKPLGILIID-----CTGN 148
DQ 14 NNFVKTTHSKSV--DSGIYLDSS-----YKMDYPMGICIIINMKNFKHKTGMSRSRG 67
QY 149 ETEL--LRDFTSLGVEVQKFLHLSMHGSLQILGACPKPHRRDPSFVCVLSKGSQS 206
DQ 68 DVADANIRETFMGKTYQVRKNDLREDLIELMDVS--KEDSKSSSFVCVILSHDEGV 126
QY 207 VYGADQTHSLPLPHIRMFMGDSCEPLAGKPMKPFICQNVVYVSDQLSDSLLEVDGPM 266
DQ 127 IYGV---INGVELKLTLPFRGDYCRSLNKPFLFIQ---ACRGELDCG--IRFDSGT- 178
QY 267 KNVEFKAKRGKGLCTVHREADFMSLCTADMSLIEGSHSSPSLYLQCLSKLR 318
DQ 179 -DERMACQK-----IPYADFLVAYSTAPGYVWRNSKDGSWFIQSLCSMLX 224

RESULT 9
ICE3_RAT STANDARD; PRT; 277 AA.
AC PS5213; P70543; P97699; G62993;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
  protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-1) (LICE) (IRP).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP MEDLINE=96358624; PubMed=8761296;
  Juan T.S.-C., Moniece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
  Fletcher F.A.;
  "Molecular characterization of mouse and rat CPP32 beta gene encoding
  a cysteine protease resembling interleukin-1 beta converting enzyme
  and CED-3.";
  Oncogene 13:749-755(1996).
RN [2]

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RP SEQUENCE OF 30-241 FROM N.A.
RC TISSUE=ovary;
RX MEDLINE=96042508; PubMed=7588240;
RA Flaws J.A., Kugu K., Tidorovich A.M., Desanti A., Tilly K.I.,
RA Hirschfield A.N., Tilly J.L.;
RT "interleukin-1 beta-converting enzyme-related proteases (IRPs) and
  mammalian cell death: dissociation of IRP-induced oligonucleosomal
  RT endonuclease activity from morphological apoptosis in granulosa cells
  of the ovarian follicle.";
  Endocrinology 136:5042-5053(1995).
RL [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97184204; PubMed=9030616;
RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
RA Rostock P. Jr., Poirier G.G., Paul S.M.;
RT "Cloning and expression of a rat brain interleukin-1beta-converting
  RT enzyme (ICE)-related protease (IRP) and its possible role in
  RT apoptosis of cultured cerebellar granule neurons.";
  J. Neurosci. 17:1561-1569(1997).
RL [4]
RP SEQUENCE OF 1-264 FROM N.A.
RA Yakovlev A.G.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in the activation cascade of caspases
  CC responsible for apoptosis execution. At the onset of apoptosis it
  CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
  CC 216-asp--gly-217 bond. Cleaves and activates sterol regulatory
  CC element binding proteins (SRBPs) between the basic helix-loop-
  CC helix leucine zipper domain and the membrane attachment domain.
  CC cleaves and activates caspase-6, -7 and -9 (by similarity).
  CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
  CC (by similarity).
  CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
  CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE
  CC BUT NOT IN KIDNEY OR TESTIS.
  CC -1- DEVELOPMENTAL STAGE: Highly expressed in neuron-enriched regions
  CC of the developing brain, but down-regulated to low levels in the
  CC adult brain.
  CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
  CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
  CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
  CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
  CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
  CC VICE VERSA (BY SIMILARITY).
  CC -1- SIMILARITY: Belongs to peptidase family C14.
  CC -----
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  CC use by non-profit institutions as long as its content is in no way
  CC modified and this statement is not removed. Usage by and for commercial
  CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
  CC or send an email to license@isb-sib.ch).
  CC -----
  DR EMBL: U49930; AAC52765.1; -
  DR EMBL: U34685; AAC52261.1; -
  DR EMBL: U84410; AAB41792.1; -
  DR EMBL: U58656; AAB02722.1; -
  DR PIR: 167437; 167437.
  DR HSSP: P42574; 1PAU.
  DR MEROPS: C14.003; -
  DR InterPro: IPR002138; ICE_P10.
  DR InterPro: IPR001309; ICE_P20.
  DR InterPro: IPR002398; Peptidase_C14.
  DR Pfam: PF00656; Peptidase_C14; 1.
  DR PRINTS: PR00376; ILIBENZYME.
  DR SMART: SM00115; CASP; 1.
  DR PROSITE: PS01122; CASPASE_CYS; 1.
  DR PROSITE: PS01121; CASPASE_HIS; 1.
  DR PROSITE: PS50207; CASPASE_P10; 1.
  DR PROSITE: PS50208; CASPASE_P20; 1.
  KW Hydrolase; Thiol protease; Zymogen; Apoptosis.

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FT PROPEP 1 9 BY SIMILARITY.
FT PROPEP 10 28 BY SIMILARITY.
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT CONFLICT 25 29 KMSDS -> QVD (IN REF. 4).
FT CONFLICT 170 170 C -> S (IN REF. 2).
FT CONFLICT 178 178 T -> A (IN REF. 2).
FT CONFLICT 182 182 M -> V (IN REF. 2).
FT CONFLICT 187 187 I -> K (IN REF. 2).
FT CONFLICT 190 190 E -> G (IN REF. 2).
FT CONFLICT 199 199 T -> S (IN REF. 2).
FT CONFLICT 211 211 D -> G (IN REF. 2).
FT CONFLICT 236 236 L -> I (IN REF. 4).
FT CONFLICT 245 245 T -> M (IN REF. 3).
SQ SEQUENCE 277 AA; 31491 MW; ADABPFI8E2507402 CRC64;

Query Match 10.3%; Score 185.5; DB 1; Length 277;
Best Local Similarity 27.5%; Pred. No. 8.36-07;
Matches 64; Conservative 37; Mismatches 93; Indels 39; Gaps 8;

QY 103 NNFRPEPVKKS-IGSEAFLEPQSIPEBRYKKKSPGLGICLIID-----CIGNETEL 151
DB 14 NNFEKTHGSKMSDGIYLDSS-----YKRDYEMWLCIINNKNFKHSTGMSARNGTD 68
QY 152 L-----LRDFTSLGYEVQKFLHLSMAGISQILGQFACMPHRDYDSFVCVLVSRGSGQSV 207
DB 69 VDAANLRTEFWALKREYVANKNDLTREELMELMDSVS-KEHSHSRSSPVCVILSHSGEVI 127
QY 208 YGVDDTHSGCLPLHNRFRFMQDSCPYLAGKPKFFIQ--NYVVSQGLEDSLLLEVDCGA 265
DB 128 FG---TNGPVDLKLITSEFRGDYCRSLTGKPKFLIIQACRGTELDGIEFDSTGDDMAC 184
QY 266 MGNVFEKAKQKRGKGLCTVHEADPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLR 318
DB 155 QK-----IPVEDFLYAVSTAPGYVMSRSGSWFIQSLCMLK 224

RESULT 10
ICB3_XENLA STANDARD; PRT; 282 AA.
AC P55866;
ID 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Caspase-3)
DE (CASP-3) (XCP32).
GN XENOPUS laevis (African clawed frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=97184166; PubMed=9030578;
RA Yaoita Y., Nakajima K.,
RT "Induction of apoptosis and CPP32 expression by thyroid hormone in a
RT myoblastic cell line derived from tadpole tail."
RL J. Biol. Chem. 272:5122-5127(1997).
CC -I- FUNCTION: Important mediator of apoptosis. At the onset of
CC apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase
CC (PARP) at a 216-ASP-Gly-217 bond (By similarity).
CC -I- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12)
CC subunits.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- MISCELLANEOUS: The subunits are derived from the precursor
CC sequence by a probable autocatalytic mechanism and probably by
CC other caspases (By similarity).
CC -I- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D89784; BAA14018.1; -.
DR HSRP: P42574; IPAU.
DR MEROPS: C14.003; -.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILI0ENZYME.
DR SMART: SM00115; CASG; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 2 APOPAIN P17 SUBUNIT.
FT CHAIN 187 282 APOPAIN P12 SUBUNIT.
FT ACT_SITE 131 131 BY SIMILARITY.
FT ACT_SITE 174 174 BY SIMILARITY.
SQ SEQUENCE 282 AA; 32124 MW; CB390E6980CAB77F CRC64;

Query Match 10.3%; Score 185.5; DB 1; Length 282;
Best Local Similarity 29.4%; Pred. No. 8.5e-07;
Matches 63; Conservative 33; Mismatches 71; Indels 47; Gaps 11;

QY 128 ERYKMSKPKGICLIID-----CIGNETEL-----LRDFTSLGYEV-----QKFLH 169
DB 46 QNRTYVPEWQCLLIINNKNFSSNMAVANGTDVALKLHETFTGLGYEVAWCNDQK--- 102
QY 170 LSMAGISQILGQFACMPF--HRDYDSFVCVLVSRGSGQ-SYVGVDQTHSGCLPLH--HIR 224
DB 103 -----SSDITGLRLKLTSEBDHSHSRSSFVCVILSHGEDSGICGV-----VPIHKNLTLD 152
QY 225 MFGDSCPYLAGKPKFFIQNYVVSQGLEDSLLLEVDCPAMKVEFYAKRGKGLCTVARE 284
DB 153 LFRGDRCKTLVGKPKFFIQ---ACKGTLDSC-IETSCSPRRRIQ-----RIIVE 201
QY 285 ADFWWSLCTADMSLLEQSHSSPSLYLQCLSQKLR 318
DB 202 ADPLVAVSTVPGYCSWRMDGMSWFIQSLCKMK 235

RESULT 11
ICB3_CR10 STANDARD; PRT; 277 AA.
ID ICB3_CR10
AC Q60431;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CSP-32) (Caspase-3) (CASP-3) (SRBP cleavage activity 1)
DE (SCA-1).
GN CRICETUS longicaudatus (Long-tailed hamster) (Chinese hamster).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10030;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=9618185; PubMed=8605870;
RA Wang X., Zielinski N.G., Yang J., Sakai J., Brown M.S.,
RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
RT CPP32 during apoptosis.";
```

EMBO J. 15:1012-1020(1996).
 -1- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. At the onset of apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-1-Gly-217 bond. Cleaves and activates sterol regulatory element binding proteins (SREBPs) between the basic helix-loop-helix leucine zipper domain and the membrane attachment domain. Cleaves and activates caspase-6, -7 and -9 (By similarity).
 -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit (By similarity).
 -1- SUBCELLULAR LOCATION: Cytoplasmic.
 -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND VICE VERSA (BY SIMILARITY).
 -1- SIMILARITY: Belongs to peptidase family C14.
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 EMBL: U27463; AAB01511.1; -.
 DR HSBP; P42574; 1PAU.
 DR MEROPS; C14.003; -.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR PRINTS; PR00376; ILIBGNZME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 9
 FT CHAIN 1 28
 FT CHAIN 29 175
 FT CHAIN 176 277
 FT ACT_SITE 121 121
 FT ACT_SITE 163 163
 FT ACT_SITE 277 277
 FT ACT_SITE 31612 31612
 FT SEQUENCE 277 AA; 31612 MW; 0BF3A4580A2828A3 CRC64;
 Query Match 10.28; Score 183.5; DB 1; Length 277;
 Best Local Similarity 27.98; Pred. No. 1.2e-06;
 Matches 67; Conservative 36; Mismatches 94; Indels 43; Gaps 9;
 96 KSLDPPNNPREEVKKS-IQSEAPFPGIPERKMKSPKPGICLID----- 144
 11 KSKT---NEVKTIHSGKSDSGIYDSS---YKMDYPMKGVITILNNKPKRSTGM 61
 145 --CIGNETEL--LRDPTSLGYEQVQLHSMGIGSQILIGQAFACMEHEDYDSPVCIVS 200
 62 TPRSGTDVDAKARETMALKEVRKNNKDLTREIYEIM-KNASKEDHKSRSFVCVILS 120
 201 RGGSGSYGVGDQHSGLPLHIRMFMGDSCEPLAKPKKFFIC--NYVSSGQGLDSSL 258
 121 HGDGVIFFGD--GPIDLKKLTSGYFGDRCRLKPKKFIIFIQACRGTELCGIEITSG 177
 259 LEVGPAMKNEVFAQKRGCLTVREARDFMSLCTADMSLLEQSHSPSLYIOCTSOQLR 318
 178 TEDMTQCK-----IPVEDPLIYASTPAGYVSWNPNRDSGMPFIQSLCSMLX 224

AC P42574; Q96AN1; Q96KP2;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 33, Last annotation update)
 DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
 DE (SCA-1).
 GN CASP3 OR CPP32
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A., AND VARIANT GLU-190.
 RC TISSUE=T-cell.
 RX MEDLINE=50744098; PubMed=7983002;
 RA Fernandez-Alnemati T., Litwack G., Alnemati E.S.;
 RT "CPP32, a novel human apoptotic protein with homology to
 RT Caenorhabditis elegans cell death protein Ced-3 and mammalian
 RT Interleukin-1 beta-converting enzyme.";
 RL J. Biol. Chem. 269:30761-30764(1994).
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=95292347; PubMed=7774019;
 RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
 RA Beutler D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;
 RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
 RT protease that cleaves the death substrate poly(ADP-ribose)
 RT polymerase.";
 RL Cell 81:801-809(1995).
 [3]
 RN SEQUENCE FROM N.A.
 RA Vallette F.M., Oliver L.J.;
 RT "Control of the activation of the procaspase-3 by a sequence located
 RT at the N-terminus of the p17 subunit";
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A., AND VARIANT GLU-190.
 RP TISSUE=Lymph;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Matulis A.K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rata S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bork S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RN SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.
 RX MEDLINE=95319529; PubMed=7596430;
 RA Nicholson D.W., Ali A., Thornberry N.A., Viallancourt J.P., Ding C.K.,
 RA Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,
 RA Munday N.A., Raju S.M., Smulson M.E., Yamin T.-T., Li V.L.,
 RA Miller D.K.;

Qy 318 RQ 319
Db 224 KQ 225

RESULT 13

ICE2_MOUSE STANDARD; PRT; 435 AA.

AC P29594; 008737;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2 protein)
DE CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA MEDLINE=95047339; PubMed=7958843;
RX Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a protein similar to the product of the Caenorhabditis elegans cell death gene ced-3 and the mammalian IL-1 beta-converting enzyme";
RT Genes Dev. 8:1613-1626(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RA MEDLINE=97190206; PubMed=9038361;
RX van de Craen M., Vandenabeele P., Declercq W., van den Brande I., van Leeuwen G., Mollema F., Schotte P., van Crickinge W., Beyaert R., Fiers W.;
RT "Characterization of seven murine caspase family members";
RT FEBS Lett. 403:61-69(1997).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=92328780; PubMed=1378265;
RX Kumar S., Tomooka Y., Noda M.;
RT "Identification of a set of genes with developmentally down-regulated expression in the mouse brain";
RT Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
RL BIOFUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. Might function by either activating some proteins required for cell death or inactivating proteins necessary for cell survival. May be important in multistep carcinogenesis.
CC -1- SUBUNIT: Heterodimer of a small and a large subunit (By similarity).
CC -1- TISSUE SPECIFICITY: High level expression seen in the embryonic CNS, liver, lung, kidney, small intestine, and hair follicles of vibrissae. Moderate expression seen in the skin, oral mucosa, skeletal muscle, submandibular gland and thymus. In the adult, it is highly expressed in spleen, lung and kidney. Moderately in the brain, heart, testis, liver. Low levels in the thymus, skeletal muscle, ovary and gut.
CC -1- DEVELOPMENTAL STAGE: During embryonic development is highly expressed in several types of mouse tissue undergoing high rates of programmed cell death such as central nervous system and kidney.
CC -1- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT THAT OF OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

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CC or send an email to license@isb-sib.ch).

DR EMBL: D28492; BAA25876.1; ALT_INIT.
DR EMBL: Y13085; CAA73527.1; ALT_INIT.
DR HSSP: P42574; 1CP3.
DR MEROPS: C14.006; -.

DR MED: MG1:97295; Casp2.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00619; CASP.1.
DR Pfam: PF00656; Peptidase_C14.1.
DR PRINTS: PRO0376; ILIBENZYM.
DR SMART: SM00114; CARD.1.
DR SMART: SM00115; CASc.1.
DR PROSITE: PS50209; CARD.1.
DR PROSITE: PS01122; CASPASE_CYS.1.
DR PROSITE: PS01121; CASPASE_HIS.1.
DR PROSITE: PS50207; CASPASE_P10.1.
DR PROSITE: PS50208; CASPASE_P20.1.
KW Hydrolyase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 152
FT CHAIN 153 316
FT CHAIN 317 435
FT CHAIN 331 435
FT DOMAIN 15 103
FT ACT_SITE 260 260
FT ACT_SITE 303 303
FT ACT_SITE 303 303
FT CONFLICT 71 71
SQ SEQUENCE 435 AA; 48896 MW; 89846AA76E7A676 CRC64;

Query Match 10.0%; Score 179.5; DB 1; Length 435;
Best Local Similarity 21.5%; Pred. No. 4,1e-06;
Matches 87; Conservative 59; Mismatches 137; Indels 121; Gaps 14;

Qy 42 LKRLNVAPDQ---DLLEKCL-KNIHRIDLTQKIQ---KYSQVQAGTSYRNVLQA- 92
Db 23 LKKNRYLAKQKLLSLLEHLLEKDIITLMEWELLQAKGSGSVVELLNLPRKGPQAF 82
Qy 93 -AIQSLKQDSNNFRPEPVKKSIOSEAFLP-----QSIPER----- 129
Db 83 DAFCEALRETRQGHLEDLITLSDIQHVLPLSCDDYDTSLPFVSCSGCPRHQURLSTD 142
Qy 130 -----YKMSKPLGICLIIDCI----- 146
Db 143 ATSHSLDNGPPCLLVKCTEPFYQAHQYLAIRLOSQPRGLALVLSNVHFTGEKDLER 202
Qy 147 -GNETE--LIRDTFTSLGYEVQKFLHLSWNGISQILGQFACMPERRDYDSFYCVLVSKGG 203
Db 203 SGSDVHTTLVTLFKLLGYNVHVLHDQTAOEQOEKLNFAQLPARVYDSCVALLSHGV 262
Qy 204 SQGVYGVDDCHSLPLHHIRBMFMGSDCPYLAGKPMFPIQ-----NY 246
Db 263 EGGIVGD--GKLLQGVYFRFLPDNANCSLQNKPMFPIQACRQEDIDRGVQDDGKNH 320
Qy 247 VVSDQQLEDSS---LLEVDGPAMK-----NVFKAQKQGLCTVHREADFWSL 291
Db 321 TQSGGCESDAGKEELMKRLPFRSDMTCGYACLKNAMRNTKSGSWYIEALTGVF--SE 379
Qy 292 CTADMSLLEQSHSPSLIYQCLSQKLRQGRGTLPGSGITSEKDM 335
Db 380 RACDMHVAADV-----LVKNVALIKEREGVAPGTEHFRCKEM 415

RESULT 14

ICE2_HUMAN STANDARD; PRT; 435 AA.

ID ICE2_HUMAN
AC P42575; P42576;
DT 01-NOV-1995 (Rel. 32, Created)

QY 264 -----PAMKNEFFKQKGLCTVHEADPFWSLCTADNLSLEQSHSPSLYLQCLSQ-- 315
 Db 318 KNAAGSPGCEESDAGKXKLPKMKLPTRSDMICGYACLTAKTAMRNTKRGSWYIEALQV 377
 QY 316 -----KLRGERGTPGSGITESHKDM 335
 Db 378 SERACDMEVADMLVKYNALIKDREGYAFGEFRCKEM 415
 RESULT 15
 ICE6_MOUSE STANDARD; PRT; 276 AA.
 ID ICE6_MOUSE
 AC 008738;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
 GN CASP6.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361;
 RA van de Craen M., Vandenaebelle P., Declercq W., van den Brande I.,
 RA van Loo G., Molemans F., Schotte P., van Cleekinge W., Beyaert R.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 FEBS Lett. 403:61-69(1997).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 responsible for apoptosis execution. Cleaves poly(ADP-ribose)
 polymerase in vitro, as well as lamins. Overexpression promotes
 programmed cell death (by similarity).
 CC -!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit
 (by similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Highly expressed in lung, liver, kidney,
 testis, and heart. Lower levels in spleen, skeletal muscle and
 brain.
 CC -!- PTM: CLEAVAGES BY CP932, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
 SUBUNITS (BY SIMILARITY).
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Y13087; CA073529.1; -.
 DR HSSP; P42574; IPNU.
 DR MEROPS; C14.005; -.
 DR MCD; MGI:1312921; Casp6.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR PRINTS; PR00376; ILIBENZTME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50209; CASPASE_P20; 1.
 DR Hydrolase; Thiol protease; Apoptosis; Zymogen.
 KM PROPEP 1 5
 FT CHAIN 6 162 CASPASE-6 SUBUNIT P18 (BY SIMILARITY).
 FT PROPEP 163 176 BY SIMILARITY.
 FT CHAIN 177 276 CASPASE-6 SUBUNIT P11 (BY SIMILARITY).

FT ACT_SITE 104 104 BY SIMILARITY.
 FT ACT_SITE 146 146 BY SIMILARITY.
 SQ SEQUENCE 276 AA; 31595 MW; 5965DB9321126B6C CRC64;
 Query Match 9.6%; Score 172.5; DB 1; Length 276;
 Best local Similarity 27.8%; Pred. No. 7.7e-06;
 Matches 62; Conservative 26; Mismatches 84; Indels 51; Gaps 8;
 QY 126 PERRYMKKPKFGICLIID-----CIGNTELLRDFTSLGYEVQK----- 167
 Db 16 PABQYMDHKRRGVALLIFNHERFFWHLTLPERGNTAARDNITRRFSDLGEVXCFNDLR 75
 QY 168 ---LHLSMHGISQLIGQFACMPEHRDYSFVCULVRGASQSVYGV-----QTHSGIPL 219
 Db 76 AEELLKIHVS-----TSHIDADCFIVLSHGKNNHVAVDAKIEIQLTGL-- 125
 QY 220 HIRRMFMDSCPYLAGKPMFFIQNYVYVDSGLDSSILEYD-----GPAMKNEFFKAQ 274
 Db 126 -----FKDPKCSQSLVGKPKFIPIQ---ACRSQHDVVPVPLDWDHQDTKLDNVT--QVD 175
 QY 275 KRGGLCTVHEADPFWSLCTADNLSLEQSHSPSLYLQCLSQCL 317
 Db 176 AASVYTLPGADPLMCGYVABGYSHREIVNGSWYIQLCEML 218

Search completed: September 8, 2004, 05:49:01
 Job time : 16 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:48:38 ; Search time 46 Seconds

(without alignments)
2386.964 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MARI6GDLKPSVSLIFLM.....ITKXDMHFSIGCILDLVL 348

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_TREMBL_25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mbc:*
9: sp_organelle:*
10: sp_phase:*
11: sp_plant:*
12: sp_ricent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rvlnus:*
17: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1774 | 98.6 | 462 | 4 | Q96TE4 |
| 2 | 1018 | 56.6 | 481 | 11 | Q812G4 |
| 3 | 471 | 26.2 | 418 | 13 | Q8UVG5 |
| 4 | 345 | 19.2 | 218 | 11 | Q9JWZ5 |
| 5 | 318.5 | 17.7 | 482 | 11 | Q9JHX4 |
| 6 | 302.5 | 16.8 | 482 | 13 | Q90WU1 |
| 7 | 277 | 15.4 | 78 | 6 | Q8M18 |
| 8 | 267 | 14.8 | 520 | 13 | Q91B62 |
| 9 | 265.5 | 14.8 | 476 | 13 | Q91B73 |
| 10 | 248.5 | 13.8 | 522 | 4 | Q81UP5 |
| 11 | 233 | 12.9 | 500 | 13 | Q91B64 |
| 12 | 214 | 11.9 | 283 | 13 | Q93A17 |
| 13 | 210.5 | 11.7 | 496 | 5 | Q81749 |
| 14 | 199 | 11.1 | 303 | 13 | Q91B66 |
| 15 | 198.5 | 11.0 | 400 | 5 | Q81P2 |
| 16 | 193.5 | 10.8 | 277 | 6 | Q95ND5 |

| | | | | | | |
|----|-------|------|-----|----|--------|--------------------|
| 17 | 192.5 | 10.7 | 318 | 13 | Q91B65 | Q91B65 xenopus lae |
| 18 | 192 | 10.7 | 277 | 6 | Q8MK15 | Q8MK15 canis faml |
| 19 | 190.5 | 10.6 | 313 | 11 | Q8CHV5 | Q8CHV5 mus musculu |
| 20 | 190 | 10.6 | 328 | 5 | Q81TP3 | Q81TP3 branchiosto |
| 21 | 189.5 | 10.5 | 277 | 6 | Q8MUT1 | Q8MUT1 felis silve |
| 22 | 187.5 | 10.4 | 302 | 13 | Q91B89 | Q91B89 oncorhynch |
| 23 | 186.5 | 10.4 | 280 | 13 | Q81B59 | Q81B59 oryzias lat |
| 24 | 184.5 | 10.2 | 182 | 6 | Q77623 | Q77623 ovis aries |
| 25 | 184 | 10.2 | 290 | 13 | Q81J58 | Q81J58 oryzias lat |
| 26 | 182.5 | 10.1 | 304 | 13 | Q93415 | Q93415 gallus gall |
| 27 | 180.5 | 10.0 | 452 | 11 | Q55194 | Q55194 rattus norv |
| 28 | 179.5 | 10.0 | 452 | 11 | Q8K241 | Q8K241 mus musculu |
| 29 | 179.5 | 10.0 | 452 | 11 | Q8C9H7 | Q8C9H7 mus musculu |
| 30 | 179 | 9.9 | 423 | 13 | Q91B67 | Q91B67 xenopus lae |
| 31 | 177.5 | 9.9 | 277 | 6 | Q8MUT3 | Q8MUT3 oryzias lat |
| 32 | 177.5 | 9.9 | 435 | 4 | Q9BUP7 | Q9BUP7 homo sapien |
| 33 | 172.5 | 9.6 | 276 | 11 | Q9D089 | Q9D089 mus musculu |
| 34 | 172.5 | 9.6 | 276 | 11 | Q9M47 | Q9M47 mus musculu |
| 35 | 172.5 | 9.6 | 280 | 13 | Q8U42 | Q8U42 figu rubrip |
| 36 | 172.5 | 9.6 | 415 | 13 | Q8U1W6 | Q8U1W6 xenopus lae |
| 37 | 172.5 | 9.6 | 419 | 13 | Q72XD2 | Q72XD2 xenopus lae |
| 38 | 172 | 9.6 | 277 | 11 | Q35397 | Q35397 rattus norv |
| 39 | 172 | 9.6 | 343 | 11 | Q9MUT6 | Q9MUT6 rattus norv |
| 40 | 170.5 | 9.5 | 312 | 4 | Q8JCM9 | Q8JCM9 figu rubrip |
| 41 | 169 | 9.4 | 312 | 4 | Q8EUT3 | Q8EUT3 homo sapien |
| 42 | 166.5 | 9.2 | 289 | 5 | Q86FL0 | Q86FL0 anopheles s |
| 43 | 165 | 9.2 | 303 | 11 | Q88550 | Q88550 rattus norv |
| 44 | 158.5 | 8.8 | 282 | 13 | Q98U18 | Q98U18 brachydanio |
| 45 | 152.5 | 8.5 | 182 | 12 | Q99CX0 | Q99CX0 bovine herp |

ALIGNMENTS

RESULT 1

| ID | Q96TE4 | PRELIMINARY; | PRT; | 462 AA. |
|----|---|--------------------------------------|------|---------|
| AC | Q96TE4 | 01-DEC-2001 (T-EMBLrel. 19, Created) | | |
| DT | 01-DEC-2001 (T-EMBLrel. 19, Last sequence update) | | | |
| DT | 01-OCT-2003 (T-EMBLrel. 25, Last annotation update) | | | |
| DE | Usurpin beta. | | | |
| OS | Homo sapiens (Human). | | | |
| CC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| CC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEHLIN-21100893; PubMed=1161814; | | | |
| RA | Hadano S., Yanagisawa Y., Skeug J., Fichter K., Nasir J., | | | |
| RA | Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A., | | | |
| RA | Ikeida J.-E., Hayden K.R., | | | |
| RT | "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2, | | | |
| RT | and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2) | | | |
| RT | critical region at chromosome 2q33-q34: Candidate genes for ALS2." | | | |
| RL | Genomics 71:200-213 (2001). | | | |
| DR | EMBL; AB038972; BAB32552.1; - | | | |
| DR | EMBL; AB038967; BAB32552.1; JOINED. | | | |
| DR | EMBL; AB038968; BAB32552.1; JOINED. | | | |
| DR | EMBL; AB038969; BAB32552.1; JOINED. | | | |
| DR | EMBL; AB038970; BAB32552.1; JOINED. | | | |
| DR | EMBL; AB038971; BAB32552.1; JOINED. | | | |
| DR | GO; GO:0016329; F:apoptosis regulator activity; IEA. | | | |
| DR | GO; GO:0030693; F:caspace activity; IEA. | | | |
| DR | GO; GO:0006955; P:apoptosis; IEA. | | | |
| DR | GO; GO:0006508; P:proteolysis and peptidolysis; IEA. | | | |
| DR | InterPro; IPR001875; ICD. | | | |
| DR | InterPro; IPR001309; ICD_p20. | | | |
| DR | InterPro; IPR002398; Peptidase_C14. | | | |
| DR | Pfam; PF00335; DED; 2. | | | |
| DR | Pfam; PF00666; Peptidase_C14; 1. | | | |
| DR | SMART; SM00115; DASC; 1. | | | |
| DR | SMART; SM00031; DED; 2. | | | |

DR PROSITE; PSS0208; CASPASE_P20; 1.
 DR PROSITE; PSS0168; DED; 2.
 SQ SEQUENCE 462 AA; 52550 MW; DAED0109CEAA7EAA3 CRC64;

Query Match 98.6%; Score 1774; DB 4; Length 462;
 Best Local Similarity 94.5%; Pred. No. 5,8e-134;
 Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYNGRGKISKEKSPFLDIIVLEKLNVAPODLLLEKCL 60
 DB 97 MAEIGEDLDKSDVSSLIPLMKDYNGRGKISKEKSPFLDIIVLEKLNVAPODLLLEKCL 156
 QY 61 KNHRIIDLKTKIQKTKOSVQAGTSYRNVLQAAIQKSLKDPSSNFR----- 106
 DB 157 KNHRIIDLKTKIQKTKOSVQAGTSYRNVLQAAIQKSLKDPSSNFR----- 216
 QY 107 ---EEPVKSIQSESAFLPOSIPERYKMSKPLGICLIIDICGNTELLRDTFTSLGY 162
 DB 217 LGAOCEPVKSIQSESAFLPOSIPERYKMSKPLGICLIIDICGNTELLRDTFTSLGY 276
 QY 163 EVQKFLHLSMHGISQILQFACMPHRDYDFVCVLVSRGSSQSVGVDTGHSGLPLHHI 222
 DB 277 EVQKFLHLSMHGISQILQFACMPHRDYDFVCVLVSRGSSQSVGVDTGHSGLPLHHI 336
 QY 223 REMFGDSCPYLAGKPKMFFIQNYVSDGQLEDSSLEVDGPAMKVEFKAQRGLCTVH 282
 DB 337 REMFGDSCPYLAGKPKMFFIQNYVSDGQLEDSSLEVDGPAMKVEFKAQRGLCTVH 396
 QY 283 RADFFWSLCTADMSLLEQSHSSPSLYIQCLSQTLROERGTIRGSGITTEKDMHSSSLGC 342
 DB 397 RADFFWSLCTADMSLLEQSHSSPSLYIQCLSQTLROERGTIRGSGITTEKDMHSSSLGC 456
 QY 343 ILLDYL 348
 DB 457 ILLDYL 462

RESULT 2

Q812G4 PRELIMINARY; PRT; 481 AA.

AC Q812G4;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE CASP8 and FADD-like apoptosis regulator.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029223; AAH29223.1; -
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR001309; ICG_P20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF01335; DED; 2.
 DR SMART; SM00115; CASc; 1.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PSS0208; CASPASE_P20; 1.
 DR PROSITE; PSS0168; DED; 2.
 SQ SEQUENCE 481 AA; 54874 MW; 43E07E2E5FA5A05 CRC64;

Query Match 56.6%; Score 1016; DB 11; Length 481;
 Best Local Similarity 62.6%; Pred. No. 2.6e-73;
 Matches 211; Conservative 41; Mismatches 67; Indels 18; Gaps 5;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYNGRGKISKEKSPFLDIIVLEKLNVAPODLLLEKCL 60
 DB 102 LMEIGEDLDNDVSLVFLTRDYTGKIAKDSFPLDIIVLEKLNVAPODLLLEKCL 161
 QY 61 KNHRIIDLKTKIQKTKOSVQAGTSYRNVLQAAIQKSLKDPSSNFR----- 109
 DB 162 KNHRIIDLKTKIQKTKOSVQAGTSYRNVLQAAIQKSLKDPSSNFR----- 220
 QY 110 ----YKSIQSESAFLPOSIPERYKMSKPLGICLIIDICGNTELLRDTFTSLGYEV 164
 DB 221 SQRTLVKTSIQSESAFLPOSIPERYKMSKPLGICLIIDICGNTELLRDTFTSLGYEV 280
 QY 165 QKFLHLSMHGISQILQFACMPHRDYDFVCVLVSRGSSQSVGVDTGHSGLPLHHI 224
 DB 281 QKFLHLSMHGISQILQFACMPHRDYDFVCVLVSRGSSQSVGVDTGHSGLPLHHI 340
 QY 225 MFMGDSCPYLAGKPKMFFIQNYVSDGQLEDSSLEVDGPAMKVEFKAQRGLCTVH 284
 DB 341 MFGDTCPSLRGPKMFFIQNYVSDGQLEDSSLEVDGPAMKVEFKAQRGLCTVH 399
 QY 285 ADFWMSLCTADMSLLEQSHSSPSLYIQCLSQTLROERGTIRGSGITTEKDMHSSSLGC 321
 DB 400 ADFWMSLCTADMSLLEQSHSSPSLYIQCLSQTLROERGTIRGSGITTEKDMHSSSLGC 436

RESULT 3

Q8UVG5 PRELIMINARY; PRT; 418 AA.

AC Q8UVG5;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Clarp1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96021435; PubMed=9380701;
 RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
 RT "ClARP, a death effector domain-containing protein interacts with caspase-8 and regulates apoptosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20373792; PubMed=10917738;
 RA Inohara N., Nunez G.;
 RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish.";
 RL Cell Death Differ. 7:509-510(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Inohara N., Nunez G.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448261; AL41007.1; -
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR001309; ICG_P20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF01335; DED; 1.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR SMART; SM00115; CASc; 1.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PSS0208; CASPASE_P20; 1.
 DR PROSITE; PSS0168; DED; 2.
 SQ SEQUENCE 418 AA; 47619 MW; C2ECB3AE571E0237 CRC64;

| RESULT 1 | Q90WU1 | PRELIMINARY; | PRT; | 482 AA. |
|----------|---|--------------|------|---------|
| ID | Q90WU1 | | | |
| AC | Q90WU1; | | | |
| DT | 01-DEC-2001 (TrEMBLrel. 19, Created) | | | |
| DT | 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) | | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | | | |
| DE | Caspase 8. | | | |
| OS | Gallus gallus (Chicken). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Archosauria; Aves; Neognathae; Galliformes; Passeriformes; Passariidae; Passarinae; | | | |
| OX | NCBI_TaxID=9031; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Barton S., Bridgman J.T., Johnson A.L.; | | | |
| RT | "Caspase-8 and -9 expression in the hen ovary."; | | | |
| RL | Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL: AY057939; AAL23700.1; - | | | |
| DR | MEROPS; C14.009; - | | | |
| DR | GO: GO:0016129; Fapoptosis regulator activity; IEA. | | | |
| DR | GO: GO:0030693; Fcaspase activity; IEA. | | | |
| DR | GO: GO:0006815; P:apoptosis; IEA. | | | |
| DR | GO: GO:0006508; P:proteolysis and peptidolysis; IEA. | | | |
| DR | InterPro: IPR001875; DED. | | | |
| DR | InterPro: IPR002138; ICE_p10. | | | |
| DR | InterPro: IPR001309; ICE_p20. | | | |
| DR | InterPro: IPR002398; Peptidase_C14. | | | |
| DR | Pfam: PF01335; DED; 2. | | | |
| DR | Pfam: PF00656; Peptidase_C14; 1. | | | |
| DR | PRINTS: PRO0376; TLICENZYM. | | | |
| DR | SMART: SM00115; CASC; 1. | | | |
| DR | SMART: SM00331; DED; 2. | | | |
| DR | PROSITE: PS01182; CASPASE_CYS; 1. | | | |
| DR | PROSITE: PS01121; CASPASE_HIS; 1. | | | |
| DR | PROSITE: PS50207; CASPASE_P10; 1. | | | |
| DR | PROSITE: PS50208; CASPASE_P20; 1. | | | |
| DR | PROSITE: PS50168; DED; 2. | | | |
| QO | SEQUENCE 482 AA; 54645 MW; 883936B6EE090B5F CRC64; | | | |

| | | | | |
|-----------------------|-------|-------------------|--------|----------------|
| Query Match | 16.8% | Score 302.5 | DB 13 | Length 482 |
| Best Local Similarity | 25.9% | Pred. No. 6,38-16 | | |
| Matches | 89 | Conservative | 67 | Mismatches 141 |
| | | | Indels | 47 |
| | | | Gaps | 10 |

| | | | |
|----|-----|--|-----|
| QY | 3 | ETGEGDLKSDVSSLIPLMKDYMGRKATSKESKFLDVLVELEKNTLVAPQDLLEKCLN | 62 |
| DB | 107 | QSEENTTKDMDKCFEFLGKELPKCKSLPETMTDVAFLMEKKGILLKEDNTLVLTCKGK | 166 |
| QY | 63 | HRIDIKTYIKYKQVQAGTSYRNVLAALCKSLDPSNNPREEPVKSKIOESAPLP | 122 |
| DB | 167 | VDKSLK-KIEYELNLLGEG-----EMLVTEGGRSSTGAPEDSALTMSSVAP | 214 |
| QY | 123 | QSTPE-----ERYKSKSPGLICLI-----DCIGN--ETELIR | 154 |
| DB | 215 | DSIGNCDOSSOLEVYKMTSRPGCLILNNNFAPKAREAVBELRMKMDRNGTHVADATR | 274 |
| QY | 155 | DTFTSLGVEVQFRLHLSNHGISQLGQFACPFBEHRYDSFVCULVARGSQSVYGVQTH | 214 |
| DB | 275 | KYFNSNIHFVAAYKQCTAEELIRNLVNNYRC-DINNNDGVCVCLILHGKKDIIYGVDOGE | 333 |
| QY | 215 | SGPLPHIRMRMGSGCPTLAGKRFMPFIQNVVSDQLEDSSLLEVD-GRMKVVEFA | 273 |
| DB | 334 | --VPIQLTSTSTGGNCOSLAKGKPEVFVQ--ACQGDAYKQGVITITSDSGEODYSLETDA | 389 |
| QY | 274 | QKRGCLTVAREADFFWMSLCTADMSLLEOSHSPELYQCUSQKL | 317 |
| DB | 390 | RQGLDQ-IPSEADFLGKTTLLQDYVYVRSBPQGTWYIQLSCQHL | 432 |

| | |
|----------|-------------------------|
| RESULT 7 | |
| Q8MD18 | |
| Q8MJ18 | PRELIMINARY; PRT 78 AA. |

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AC  Q8MU18; 08MU18; 01-OCT-2002 (TrEMBLrel. 22, Created)
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Qy  YRVVLOALQKSLKPKNSNNR-----DEPPYKSLQSEAFLLPSIPE 127
Db  1 YRVVLOALQKSLKPKNSNNRFLHNGRSKQRLKEQLGTQCEPVKTSIQSEAFLLPSIPE 60
Qy  128 ERYKMSKRLGICLIIDC 145
Db  61 ERYKMSKRLGICLIIDC 78

RESULT 8
Q91B62
Q91B62 PRELIMINARY; PRT; 520 AA.
AC Q91B62;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-10.
GN XCPASPASB-10.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
CC Xenopodinae; Xenopus.
CX NCBI_taxid=8355;
CK 11
RN
RP SEQUENCE FROM N.A.
RA MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yacita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
   family."
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB028173; BAA94751.1; -.
DR HSP; Q15806; 1QDU.
DR GO; GO:0016129; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p30.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED_2.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILHICENZYME.
DR SMART; SMO0115; CASc; 1.
DR SMART; SMO0031; DED; 2.

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DR InterPro; IPR002398; peptidase_c14

DR PROSITE; PS01122; CASPASE_CYS; 1.

DR PROSITE, PS01121, CASPASE_HIS; 1.
 DR PROSITE, PS0207, CASPASE_P10; 1.
 DR PROSITE, PS0208, CASPASE_P20; 1.
 DR PROSITE, PS0168, DED; 2.
 KW PROTEASE.
 SQ SEQUENCE 522 AA; 58993 MW; 34847E07B3DFA688 CRC64;

Query Match 13.8%; Score 248.5; DB 4; Length 522;
 Best Local Similarity 25.3%; Pred. No. 1.5e-11;
 Matches 91; Conservative 60; Mismatches 154; Indels 55; Gaps 11;

QY 3 EIGEDLDKSDVSLIFLMDYMGKGIKSKESFLDLVVELEKLVAPDQDLLE-----57
 DB 121 ELSEGISDENLKMFLFKDLPK-----TENTSLSLFLAFLEKQKIDEDLTLELDCT 176
 QY 58 ---KLLKNIHRIDLTKTQ-----KKQSVQ-----AGTSRYNLQALQKSLKDP- 101
 DB 177 VVFKLLRNIEKKYKKEKAIQIVTPVDKEASVQGEELVQTDVKTFLLEALPQESWQNH 236
 QY 102 -----SNNFREBPVKKSIQSEAFLPQSIPEER-----YKMKSKPLIGLII-----143
 DB 237 AGSNRNKATNGAPSLVSKMGQASANTLNSETSKRAAYRNKRNRHGLCVIYNHSTFS 296
 QY 144 --DCIG--NETELADFTSLGYEVQKFLHLSMHGISQLIGQFACMPERHDYDSFVCVLV 199
 DB 297 LKDRGGRKDAEILSHVQWLGFTVHIHNVTKVEMEMVLQKQKNPAHADGCFVFCIL 356
 QY 200 SRGGSQSYGVQDQTHSGFLPHIRKFMGDSCEPLACKPMFLQNYVVSQGLDSSLL 259
 DB 357 THGRFGAVYSSDE--ALPIREIMSHFTALQCPFLAKPKLFFIQ--ACGSEITQPSVSI 412
 QY 260 EVDGPGMKNVVEFKQKRGICTVREADFWSICTADMSLLEQSHSPSLYLQCLSQKLRQ 319
 DB 413 EADANPEQAPTSIQD-----SLPAADFLIGLAIIVPGVSRFVREGSVNVIQSLCNHLAK 468

RESULT 11
 Q91B64 PRELIMINARY; PRT; 500 AA.
 AC Q91B64;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE Caspase-8.
 GN XCASPASE-8.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RX MEDLINE=20209426; PubMed=10744739;
 RA Nakajima K., Takahashi A., Yaoita Y.;
 RT "Structure, expression and function of the Xenopus laevis caspase
 family";
 RL J. Biol. Chem. 275:10484-10491 (2000).
 DR EMBL; AB038171; BAA94749.1; -.
 DR MEROPS; C14.009; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. .); IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR InterPro; IPR000226; Interleukin_7_9.
 DR InterPro; IPR002398; Peptidase_C14.

DR Pfam; PF01335; DED; 2.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBENZYM.
 DR SMART; SM00115; CASG; 1.
 DR SMART; SM00031; DED; 2.
 DR PROSITE, PS01122; CASPASE_CYS; 1.
 DR PROSITE, PS01121; CASPASE_HIS; 1.
 DR PROSITE, PS0207; CASPASE_P10; 1.
 DR PROSITE, PS0208; CASPASE_P20; 1.
 DR PROSITE, PS0168; DED; 2.
 DR PROSITE, PS00255; INTERLEUKIN_7_9; 1.
 SQ SEQUENCE 500 AA; 57623 MW; AE138D4145108AE2 CRC64;

Query Match 12.9%; Score 233; DB 13; Length 500;
 Best Local Similarity 24.3%; Pred. No. 2.5e-10;
 Matches 84; Conservative 67; Mismatches 148; Indels 46; Gaps 13;

QY 3 EIGEDLDKSDVSLIFLMDYMGKGIKSKESFLDLVVELEKLVAPDQDLLEKCKLN 62
 DB 119 DISQGLSKKEVEDLKYLD--LSTAK-TENAGILFLFLEKVGKLTHPDDQLKHLDEL 175
 QY 63 IHRIDLTKTQKTKQKQSVQAGTSYRN-----VLQALQKSLKDSNNFREBPVKS 113
 DB 176 IGCKNLSRNIEDYERISEADNHRPENLPDLFEKISVQEBQVCTAQEBFNEQRTPOET 235
 QY 114 IOSEAFLPQS--IPEERYKMKSKPLIGLII-----DC-----IGNETEL 152
 DB 236 --ESDYQCPQOHSHMLLETYLEKPHMGCVIINNYDPKARSQCKXTDRGTXKDAE 293
 QY 153 LRLFTSLGYEVQKFLHLSMHGISQLIGQFACMPERHDYDSFVCVLVSRGGSQSYGVQD 212
 DB 294 ITRIFNARGYITREHDLTAANIQTLEWYS-KDHAEDSFVCFILSHGGVGTCCGDG 352
 QY 213 THSGFLPHIRKFMGDSCEPLACKPMFLQNYVVSQGLDSSLLVDGPGMKNVVEFK 272
 DB 353 EE--VEIKRLTKTFNQDQGRSLINKPKLFFIQ--ACQK-BSHPKVMD--DTSRYE 403
 QY 273 AQKRGICTVREADFWSICTADMSLLEQSHSPSLYLQCLSQKLRQ 317
 DB 404 PDANG--SHLPLEADFLTAFAVEDYTSLSHRENGSIYIQLCKAL 447

RESULT 12
 Q93417 PRELIMINARY; PRT; 283 AA.
 AC Q93417;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE Caspase-3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RX MEDLINE=62589-598 (2000).
 DR EMBL; AF083029; AAC32602.1; -.
 DR HSP; P42574; IPAU.
 DR MEROPS; C14.003; -.
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBENZYM.
 DR SMART; SM00115; CASG; 1.

RESULT 15

Q8ITP2 PRELIMINARY; PRT; 400 AA.
AC Q8ITP2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE AmphicASP-6.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RA Bayasas J.R., Yuste V.J., Benito E., Garcia-Fernandez J.,
RA Comella J.X.,
RT "Isolation of AmphicASP-6, an amphioxus (Branchiostoma floridae)
RT caspase-6 homolog containing a Eyrin prodomain."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF412336; AAN45850.1; -
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICS_P10.
DR InterPro; IPR001309; ICS_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILHCENZYME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 400 AA; 44309 MW; 5C3B1B813E73DFAE CRC64;

Query Match

11.0%; Score 198.5; DB 5; Length 400;

Best Local Similarity 26.8%; Pred. No. 1,1e-07;
Matches 73; Conservative 44; Mismatches 116; Indels 39; Gaps 10;

QY 76 KQSVQAGTSTRNVIQAIQKSLKDPNNFREPVKYSIQSEAFLEPQSIPEERYKMKSK 135
DB 93 KEVCLGPGHAEKVTVDSSQEQODEPDAPIVSIARRAPQAE--LIQDLPS--YNNAP 148
QY 136 PLGICLLIDICIGNE-----TEL-----LRDFTSLGVEYQKFLHSMGISOI 178
DB 149 QRGDLCLVPD--NEEFHTTKMNRNRSGSHVDAGNLKVMFEGLGFSVEVLKDKETITRIQI 205
QY 179 LQGFACMPHRDYDSFVCLVSRGQSQSVYGVQTHSGLPPLHRIKRVFMGDSQPYLAGKP 238
DB 206 LHSALKYDHSQDQCFVFLSHGEDGNIYGVNGT--VPIKETIDVFRADRTSLKGP 262
QY 239 KMFETQ-----NYVVSQDLQEDSSILEVDGA--MKNVKFAKRGGLCTHREADPFMSL 291
DB 263 KLEFIQACRGAKHEIPVEPLDEPDGLBSGSAEPMDVVDAGVRP---TLPAGADFLXAY 318
QY 292 CTADMSLLEQSHSPSLYLQCLISQLRQERGT 323
DB 319 SVSEGFYSHRDVTNGSWYVQDLCAALKQ-HGT 349

Search completed: September 8, 2004, 05:51:28
Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2004, 06:24:47 / Search time 40 Seconds

(without alignments)
836.866 Million cell updates/sec

Title: US-10-713-208-6

Perfect score: 1800

Sequence: 1 MAEIGDLKSDVSSLIFLM.....ITBSKDXHFFSLGICLLDVL 348

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 180989

Minimum DB seq length: 0

Maximum DB seq length: 348

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|--------|--------------------|
| 1 | 184.5 | 10.2 | 212 | 2 | 167437 | cysteine proteinas |
| 2 | 184.5 | 10.2 | 277 | 2 | S64710 | cysteine proteinas |
| 3 | 184.5 | 10.2 | 277 | 2 | JCS410 | CP32 protein - mo |
| 4 | 183.5 | 10.2 | 277 | 2 | AS5315 | cysteine proteinas |
| 5 | 169 | 9.4 | 312 | 2 | BS4821 | apoptosis regulato |
| 6 | 149.5 | 8.3 | 182 | 2 | 167436 | interleukin-1-beta |
| 7 | 124.5 | 6.9 | 311 | 2 | BS6084 | interleukin-1-beta |
| 8 | 122 | 6.8 | 241 | 2 | T30761 | hypothetical prote |
| 9 | 120 | 6.7 | 263 | 2 | C56084 | interleukin-1-beta |
| 10 | 94.5 | 5.2 | 344 | 2 | B70136 | flagellar motor sw |
| 11 | 89.5 | 5.0 | 184 | 2 | A71230 | hypothetical prote |
| 12 | 89.5 | 5.0 | 285 | 2 | AE0230 | Gnfr-family probab |
| 13 | 88.5 | 4.9 | 168 | 1 | A64478 | hypothetical prote |
| 14 | 88.5 | 4.9 | 208 | 2 | AS6912 | PAAD protein - hum |
| 15 | 86.5 | 4.8 | 259 | 2 | A71890 | hydroxyethylthiaz |
| 16 | 85 | 4.7 | 293 | 2 | JC7561 | 3(or 17)beta-hydro |
| 17 | 84 | 4.7 | 247 | 2 | T33654 | hypothetical prote |
| 18 | 84 | 4.7 | 319 | 2 | B86615 | pp-loop type ATPas |
| 19 | 84 | 4.7 | 319 | 2 | E72809 | Mes/YC62 family |
| 20 | 83.5 | 4.6 | 301 | 2 | A70335 | hypothetical prote |
| 21 | 82.5 | 4.6 | 324 | 2 | C83695 | quinone oxidoreduc |
| 22 | 82 | 4.6 | 265 | 2 | S70247 | hypothetical prote |
| 23 | 81.5 | 4.5 | 252 | 2 | AE1985 | hesa protein limpo |
| 24 | 81.5 | 4.5 | 266 | 2 | S11900 | hypothetical prote |
| 25 | 81 | 4.5 | 168 | 2 | T01482 | hypothetical prote |
| 26 | 81 | 4.5 | 273 | 2 | S65215 | hypothetical prote |
| 27 | 81 | 4.5 | 317 | 2 | B71922 | probable sideropho |
| 28 | 81 | 4.5 | 318 | 2 | E70117 | membrane fusion pr |
| 29 | 81 | 4.5 | 324 | 2 | F64592 | hypothetical prote |

| | | | | | | |
|----|------|-----|-----|---|--------|----------------------|
| 30 | 80.5 | 4.5 | 171 | 2 | S55668 | hypothetical prote |
| 31 | 80.5 | 4.5 | 292 | 2 | UC7517 | caspase-14/a - hum |
| 32 | 80.5 | 4.5 | 242 | 1 | A40650 | UTP-glucose-1-phos |
| 33 | 80.5 | 4.5 | 308 | 2 | B97263 | tagatose-6-phospha |
| 34 | 80.5 | 4.5 | 313 | 2 | S51754 | NSP3 protein - por |
| 35 | 80.5 | 4.5 | 331 | 2 | A71870 | integrase/recombin |
| 36 | 80 | 4.4 | 217 | 2 | H90217 | SSU ribosomal prot |
| 37 | 80 | 4.4 | 238 | 2 | C69157 | recombinase - Meth |
| 38 | 80 | 4.4 | 279 | 2 | H97934 | transcription anti |
| 39 | 80 | 4.4 | 314 | 2 | T25372 | hypothetical prote |
| 40 | 79.5 | 4.4 | 184 | 2 | T07440 | H+-transporting tw |
| 41 | 79.5 | 4.4 | 267 | 2 | A33122 | dojicetyl-phosphate |
| 42 | 79.5 | 4.4 | 313 | 2 | S51753 | NSP3 protein - por |
| 43 | 79.5 | 4.4 | 315 | 2 | C82425 | sensor histidine kin |
| 44 | 79 | 4.4 | 197 | 2 | G64329 | anthranilate synth |
| 45 | 79 | 4.4 | 279 | 2 | A95067 | transcription anti |

ALIGNMENTS

RESULT 1
167437
cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C/Accession: 167437
R/Flaws: J.A.; Kugu, K.; Tybovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfeld, A.N.; Til
Endocrinology 136, 5042-5053, 1995
A/Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
nula cells of the ovarian follicle.
A/Reference number: 153300; MUID:96042508; PMID:7588240
A/Accession: 167437
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-212 <RBS>
A/Cross-references: EMBL:U34685; NID:g1004370; PIDD:AA652261.1; PID:g1004371
C/Keywords: cysteine proteinase; hydrolase

Query Match 10.2%; Score 184.5; DB 2; Length 212;
Best local similarity 29.1%; Pred. No. 7.2e-07;
Matches 60; Conservative 36; Mismatches 81; Indels 29; Gaps 8;

| | | | |
|----|-----|---|--|
| QY | 127 | EEBYKXKSKPLDICIILID-----CIGNETEL---IRDFTSGYGVQKFLISM 172 | |
| DB | 5 | DSGYKMDYEMGLCIINKNFKSTGMSARNGVDADANIRETFMALKYEVNRKNDLTR 64 | |
| QY | 173 | HGISQILGFCACMPERRDVPVCLVARGSQSYGVDTSGPLHIRMFWGDCSP 232 | |
| DB | 65 | BEIMEIMDSVS-KEDHSKRSSFVCVILSHGDEGVIFG---TNGPVDLKKLTSFRGDYCR 120 | |
| QY | 233 | YLAGKPMFFIIONVYVSDQLEDSILLEVDPAMKNVEFKQKRGCLTVHREADFFWSLC 292 | |
| DB | 121 | SLTGKPKLFIIQ---ACRGTEDSG-IETDSGADDDV--ACQKRV-----EADFLVYS 169 | |
| QY | 293 | TADMSLLBQSHSSPSVYQCLSQKLR 318 | |
| DB | 170 | SAPGYVSRNRSRGSMFIQSLCAMLK 195 | |

RESULT 2
S64710
cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
C/Species: Citreululus griseus (Chinese hamster)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C/Accession: S64710; S72395
R/Flaws: X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
EMBO J. 15, 1012-1020, 1996
A/Title: Cleavage of sterol regulatory element binding proteins (SRBPs) by CPP32 during
A/Reference number: S64710; MUID:96183185; PMID:8605870
A/Accession: S64710
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA

A:Residues: 1-277 <MAN>
 A:Cross-references: EMBL:U27463
 R:Wang, X.
 Submitted to the EMBL Data Library, May 1995
 A:Reference number: S72395
 A:Accession: S72395
 A:Molecule type: mRNA
 A:Residues: 1-79, 'A', 81-146, 'Y', 148-277 <MAN>
 A:Cross-references: EMBL:U27463; NID:91244443; PDB:AA01511.1; PID:g1244444
 C:Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 10.2%; Score 184.5; DB 2; Length 277;
 Best Local Similarity 27.9%; Pred. No. 1e-06;
 Matches 67; Conservative 36; Mismatches 94; Indels 43; Gaps 9;

QY 96 KSLDPSNNPREEPVKS-IOESAFIPQSIPEERYKMKSPGICLIID----- 144
 DB 11 KSIR---NFEVKTIHGSKMSDGIYLDSS---YKMDYPEMGVCIITNNKPKFKSTGM 61
 QY 145 --CIGNETEL--LRDTFTSLGVEYQKFLHSMHGISOIGQFACMPEHRDYDSFVCYLV 200
 DB 62 TPBSTVDPAKAKLETFTNNLKTYVRNKNIDLREIIVELM-KNKSXEDSKRSSFVCYLV 120
 QY 201 RGSOSYGVVDQTHSGPLHHIRRMFGDSCPYLAGKPKFFIQ--NYVSDGQLEDSSL 258
 DB 121 HGDGVIFGTD---GPIDLKLTIFRGDRCRSLTGPKFLIIQACRGTELDGIEITDSG 177
 QY 259 LEVDGPAKKNVEFAKQKGLCTVHREADFWSLCTADMSLLEQSHSSPSLYLQCLSQKLR 318
 DB 178 TEDVTCK-----IPEADFLVAYSTAPGYYSWNSKSGSWFIQSLCSMLK 224

RESULT 3
 JCS410
 CP32 protein - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
 C:Accession: JCS410
 R: Mukasa, T.; Urae, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
 Biochem. Biophys. Res. Commun. 231, 170-174, 1997
 A:Title: Specific expression of CP32 in sensory neurons of mouse embryos and activation
 A:Reference number: JCS410; MUID:97224429; PMID:9070890
 A:Accession: JCS410
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-277 <MO>
 A:Cross-references: DDBJ:D86352
 A:Experimental source: embryo
 C:Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 10.2%; Score 184.5; DB 2; Length 277;
 Best Local Similarity 28.9%; Pred. No. 1e-06;
 Matches 67; Conservative 35; Mismatches 93; Indels 37; Gaps 11;

QY 103 NNPREEPV--KKSIOESAFIPQSIPEERYKMKSPGICLI-----DCIGN 148
 DB 14 NNFVKTIHGSKSV-DSGIYLDSS---YKMDYPEMGVCIITNNKPKFKSTGMSRSST 67
 QY 149 ETEL--LRDTFTSLGVEYQKFLHSMHGISOIGQFACMPEHRDYDSFVCYLVSGQSOS 206
 DB 68 DVDANLRETFMGKLYVRNKNIDLREIIVELMDVS-KEDHSKRSSFVCYLISHGDEGV 126
 QY 207 VYGVVDQTHSGPLHHIRRMFGDSCPYLAGKPKFFIQ--NYVSDGQLEDSSLLEVDGPAM 266
 DB 127 IFG---TNGPVDLKLTIFRGDRCRSLTGPKFLIIQ--ACRGTELDGIEITDS 178
 QY 267 KNVEFAKQKGLCTVHREADFWSLCTADMSLLEQSHSSPSLYLQCLSQKLR 318
 DB 179 -DEEMACQK-----IPEADFLVAYSTAPGYYSWNSKSGSWFIQSLCSMLK 224

RESULT 4
 AS5315

cysteine proteinase (EC 3.4.22.-) CP32 precursor - human
 N:Alternate names: cysteine proteinase CP32
 C:Species: Homo sapiens (man)
 C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
 C:Accession: A55315; S58899; I39005
 R:Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
 J. Biol. Chem. 269, 30761-30764, 1994
 A:Title: CP32, a novel human apoptotic protein with homology to Caenorhabditis elegans
 A:Reference number: A55315; MUID:95074098; PMID:7983002
 A:Accession: A55315
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-277 <PER>
 A:Cross-references: GB:U13737; NID:5561665; PDB:AAA5015.1; PID:g561666
 R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant,
 J.; Yu, V.L.; Miller, D.K.
 Nature 376, 37-43, 1995
 A:Title: Identification and inhibition of the ICE/ced-3 protease necessary for mamma
 A:Reference number: S58899; MUID:95319529; PMID:7596430
 A:Accession: S58899
 A:Molecule type: protein
 A:Residues: 28-46; 116-189, 'E', 191-193 <NIC>
 R:Twari, M.; Qian, L.T.; O'Rourke, K.; Deeneyers, S.; Zeng, Z.; Beidler, D.R.; Poit
 Cell 81, 601-609, 1995
 A:Title: Yama/CP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
 A:Reference number: A56924; MUID:95292347; PMID:7774019
 A:Accession: I39005
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-189, 'E', 191-277 <RES>
 A:Cross-references: EMBL:U26943; NID:9857568; PDB:AA74929.1; PID:g857569
 C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 10.2%; Score 183.5; DB 2; Length 277;
 Best Local Similarity 26.4%; Pred. No. 1.2e-06;
 Matches 64; Conservative 41; Mismatches 100; Indels 37; Gaps 7;

QY 98 LKDPNNPREEPVKS-IOESAFIPQSIPEERYKMKSPGICLIID----- 144
 DB 1 MENTENSVSKSKINLEPKTIHGSKMSDGIYLDSSYKMDYPEMGVCIITNNKPKFKSTG 60
 QY 145 --CIGNETEL--LRDTFTSLGVEYQKFLHSMHGISOIGQFACMPEHRDYDSFVCYLV 199
 DB 61 MTRSGTVDPAANLRETFNNLKTYVRNKNIDLREIIVELMDVS-KEDHSKRSSFVCYL 119
 QY 200 SRSOSYGVVDQTHSGPLHHIRRMFGDSCPYLAGKPKFFIQ--NYVSDGQLEDSSL 257
 DB 120 SHEEEGIIIG--TNGPVDLKLTIFRGDRCRSLTGPKFLIIQACRGTELDGIEITDS 176
 QY 258 LLEVDGPAKKNVEFAKQKGLCTVHREADFWSLCTADMSLLEQSHSSPSLYLQCLSQKLR 317
 DB 177 GVDDWACHK-----IPEADFLVAYSTAPGYYSWNSKSGSWFIQSLCSMLK 223
 QY 318 RQ 319
 DB 224 KQ 225

RESULT 5
 B54821
 apoptosis regulator ICH-1, suppressive form S - human
 C:Species: Homo sapiens (man)
 C>Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 C:Accession: B54821
 R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
 Cell 76, 739-750, 1994
 A:Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulat
 A:Reference number: A54821; MUID:94373811; PMID:8087842
 A:Accession: B54821
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-312 <MAN>
 A:Cross-references: GB:U10322

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OM protein - protein search, using sw model

Run on: September 8, 2004, 06:05:07 / Search time 25 Seconds
(without alignments)
724.817 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDLPKSDVSLIFLM.....ITEXKDMFSSIGCILDLVL 348

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues
Total number of hits satisfying chosen parameters: 83046

Minimum DB seq length: 0
Maximum DB seq length: 348

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 199 | 11.1 | 293 | 1 | ICB6_HUMAN |
| 2 | 188.5 | 10.5 | 277 | 1 | P55212 homo sapien |
| 3 | 185.5 | 10.3 | 277 | 1 | ICB3_MOUSE |
| 4 | 185.5 | 10.3 | 282 | 1 | ICB3_XENLA |
| 5 | 183.5 | 10.2 | 277 | 1 | ICB3_CRILLO |
| 6 | 183.5 | 10.2 | 277 | 1 | ICB3_HUMAN |
| 7 | 172.5 | 9.6 | 276 | 1 | ICB6_MOUSE |
| 8 | 167.5 | 9.3 | 303 | 1 | ICB2_HUMAN |
| 9 | 167.5 | 9.3 | 312 | 1 | ICB2_RAT |
| 10 | 163.5 | 9.1 | 303 | 1 | ICB7_MOUSE |
| 11 | 162.5 | 9.0 | 303 | 1 | ICB7_MESAU |
| 12 | 150 | 8.3 | 333 | 1 | ICB1_DROME |
| 13 | 149.5 | 8.3 | 339 | 1 | ICB1_DROME |
| 14 | 142.5 | 7.9 | 299 | 1 | ICB1_SPOFR |
| 15 | 122 | 6.8 | 241 | 1 | ICB1_MCV1 |
| 16 | 94.5 | 5.2 | 344 | 1 | ICB1_BORBU |
| 17 | 91.5 | 5.1 | 216 | 1 | ICB1_BACCR |
| 18 | 91.5 | 5.1 | 248 | 1 | ICB1_ECHGR |
| 19 | 91.5 | 5.1 | 248 | 1 | ICB1_ECHMU |
| 20 | 91.5 | 5.1 | 257 | 1 | ICB1_MOUSE |
| 21 | 89.5 | 5.0 | 184 | 1 | ICB1_PRRHO |
| 22 | 88.5 | 4.9 | 168 | 1 | ICB1_METJA |
| 23 | 88.5 | 4.9 | 208 | 1 | ICB1_HUMAN |
| 24 | 86.5 | 4.8 | 259 | 1 | ICB1_HELPF |
| 25 | 86.5 | 4.8 | 290 | 1 | ICB1_DROME |
| 26 | 85.5 | 4.8 | 209 | 1 | ICB1_STR33 |
| 27 | 85.5 | 4.8 | 217 | 1 | ICB1_BACCA |
| 28 | 84 | 4.7 | 345 | 1 | ICB1_TETHA |
| 29 | 83.5 | 4.6 | 301 | 1 | ICB1_AOUAR |
| 30 | 82.5 | 4.6 | 216 | 1 | ICB1_FALSO |
| 31 | 82 | 4.6 | 206 | 1 | ICB1_MYCPE |
| 32 | 82 | 4.6 | 255 | 1 | ICB1_ANAFA |
| 33 | 81.5 | 4.5 | 252 | 1 | ICB1_ANASP |

| | | | | | |
|----|------|-----|-----|---|------------|
| 34 | 81.5 | 4.5 | 280 | 1 | ICB1_ARATH |
| 35 | 80.5 | 4.5 | 171 | 1 | ICB1_HSV2 |
| 36 | 80.5 | 4.5 | 242 | 1 | ICB1_HUMAN |
| 37 | 80.5 | 4.5 | 242 | 1 | ICB1_BACCU |
| 38 | 80 | 4.4 | 244 | 1 | ICB1_ECHMU |
| 39 | 80 | 4.4 | 244 | 1 | ICB1_PASMT |
| 40 | 79.5 | 4.4 | 184 | 1 | ICB1_PINTH |
| 41 | 79.5 | 4.4 | 267 | 1 | ICB1_YEAST |
| 42 | 79 | 4.4 | 197 | 1 | ICB1_METJA |
| 43 | 79 | 4.4 | 205 | 1 | ICB1_MOUSE |
| 44 | 79 | 4.4 | 308 | 1 | ICB1_METJA |
| 45 | 78.5 | 4.4 | 214 | 1 | ICB1_SULSO |

ALIGNMENTS

RESULT 1
ICB6_HUMAN STANDARD; PRT; 293 AA.
ID ICB6_HUMAN
AC P55212; Q9BOE7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
GN CASP6 OR MCH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RC TISSUE=T-cell;
RX MEDLINE=95316841; PubMed=7796386;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT "Mch2, a new member of the apoptotic Ced-3/Ice cysteine protease gene family".
RT Cancer Res. 55:2737-2742(1995).
RL
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witzak L.A., Nickerson D.A.;
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sapietson M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmitt J., Myers R.M.,
RA Butterfield V.S.N., Krzywicki M.I., Skalska U., Smaluk D.E.,
RA Schmeck A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP PROCESSING.
RC TISSUE=Lymphocytes;
RX MEDLINE=97059171; PubMed=8900201;
RA Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,

| QY | 153 | LDSTTSGLGYEYOKF-----LHLSMHGSIQILGQACMP | BEHRDYSFVCLVSRGSGQ | 205 |
|----|-----|--|----------------------|-----|
| Db | 74 | LIRRRSDGFEVFKCNNDIKAMELLIKTHEVSTV-----SHADAD | CVCFVLSHGREN | 125 |
| QY | 206 | SYGYVD-----QTHSGPLPHIRMPMGDSCPTLAKPKKFFIQ----- | NYV | 248 |
| Db | 126 | HYAYDAKIEIQTTLGL-----FKGDGCHSLVSKPKIFIIQACRGNQ | CHDVPIPLDV | 177 |
| QY | 249 | SDGQEE--DSSLLEVDGPFAMGVEFFKQKRGKGLCTVHREAD | FFWSLCTADMSLLEQSHSSP | 306 |
| Db | 178 | VNQHEKLDITNTEVDAS-----VYTLBAGADFLMCVSVAGYSHRETVG | | 225 |
| QY | 307 | SLYDQCLSQKL | 317 | |
| Db | 226 | SWYIDLCSEML | 236 | |

RESULT 2

| ID | ICE3_MOUSE | STANDARD: | PRT: | 277 AA. |
|----|---|-----------|------|---------|
| AC | P70677; 008668; Q90W14; | | | |
| DT | 01-NOV-1997 (rel. 35; Created) | | | |
| DT | 01-NOV-1997 (rel. 35; Last sequence update) | | | |
| DT | 15-MAR-2004 (rel. 43; Last annotation update) | | | |
| DE | Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama | | | |
| DE | protein) (COP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1) | | | |
| DE | (SCA-3) (LICE) (LICE) | | | |
| GN | CASP3 OR CPP32. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI TaxId=10090; | | | |
| RA | Ulan T.S.-C, McNamee I.K., Jenkins N.A., Gilbert D.J., Copeland N.G., | | | |
| RA | Fletcher F.A., | | | |
| RT | Molecular characterization of mouse and rat CPP32 beta gene encoding | | | |
| RT | a cysteine protease resembling interleukin-1 beta converting enzyme | | | |
| RT | and CED-3." | | | |
| RL | Oncogene 13:749-755(1996). | | | |
| RL | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RP | MEDLINE=97224429; PubMed=9070890; | | | |
| RX | Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T., | | | |
| RA | "Specific expression of CPP32 in sensory neurons of mouse embryos and | | | |
| RT | activation of CPP32 in the apoptosis induced by a withdrawal of | | | |
| RT | NGF." | | | |
| RL | Biochem. Biophys. Res. Commun. 231:770-774(1997). | | | |
| RL | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RP | STRAIN=GH/An. | | | |
| RX | MEDLINE=97130206; PubMed=9039361; | | | |
| RA | van de Craen W., Vandenaebelle P., Declercq W., van den Brande I., | | | |
| RA | van Loo G., Moilemans F., Schotte P., van Clefinge W., Beyaert R., | | | |
| RA | Fiers W.; | | | |
| RT | "Characterization of seven murine caspase family members." | | | |
| RL | FEBS Lett. 403:61-69(1997). | | | |
| RL | [4] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RP | STRAIN=FVB/N; TISSUE=Mammary gland; | | | |
| RX | MEDLINE=97130206; PubMed=9039361; | | | |
| RA | Straussberg R.L., Reingold E.A., Grouse L.H., Derge J.G., | | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schlier G.D., | | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang S.I., Hsien F., | | | |

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.C., Hale S., Garcia A.M., Gay L.J., Hultj S.W.,
 RA Fanev J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.C.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttenfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN (6).
 RA SEQUENCE OF 58-277 FROM N.A.
 RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
 RA Fortin J.-P., Sekaly R.-P.;
 RA "Multiple pathways of apoptosis converging on the CPP32 protease";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves IL-1 beta between an Asp and an Ala, releasing the mature
 CC cytokine which is involved in a variety of inflammatory processes.
 CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highest expression in brain, skeletal muscle and
 CC kidney and heart. Lower expression in brain, skeletal muscle and
 CC testis.
 CC -1- PM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROPEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROPEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -----
 CC EMBL: U54803; AAC52768.1; -;
 CC EMBL: U54802; AAC52768.1; JOINED.
 CC EMBL: U49929; AAC52764.1; -;
 CC EMBL: D86352; BAA21727.1; -;
 CC EMBL: Y13086; CAA73528.1; -;
 CC EMBL: U19522; AAC53196.1; -;
 CC EMBL: BC038825; AAH38825.2; -;
 CC EMBL: U63720; AAD09504.1; -;
 CC PIR: JCS410; JCS410.
 CC HSSP: P42574; IPAU.
 CC MEROPS: C14.003; -;
 CC MGd: MGd107739; Casp3.
 CC InterPro: IPR002138; ICE_P10.
 CC InterPro: IPR001309; ICE_P20.
 CC InterPro: IPR002398; Peptidase C14.
 CC Pfam: PF00656; Peptidase C14; 1.
 CC PRINTS: PR00376; IL1BENZIME.
 CC SMART: SMO0115; CASC.1.
 CC PROSITE: PS01122; CASPASE_C15; 1.
 CC PROSITE: PS01121; CASPASE_HIS; 1.
 DR

DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 KM Hydroxylase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 9
 FT PROPEP 10 28 BY SIMILARITY.
 FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
 FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 121 121 BY SIMILARITY.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT CONFLICT 17 17 E -> G (IN REF. 2).
 FT CONFLICT 51 51 N -> T (IN REF. 2).
 FT CONFLICT 63 63 SRS -> ARN (IN REF. 6).
 FT CONFLICT 84 84 Q -> E (IN REF. 2).
 FT CONFLICT 95 95 D -> E (IN REF. 2).
 FT CONFLICT 97 97 L -> F (IN REF. 2).
 FT CONFLICT 128 128 Y -> F (IN REF. 2).
 FT CONFLICT 135 135 E -> D (IN REF. 2).
 FT CONFLICT 231 231 E -> Q (IN REF. 6).
 FT CONFLICT 262 262 I -> F (IN REF. 6).
 SQ SEQUENCE 277 AA; 31474 MW; CE91598F7482605 CRC64;
 Query Match 10.5%; Score 188.5; DB 1; Length 277;
 Best Local Similarity 28.9%; Pred. No. Se-07; 92; Indels 37; Gaps 11;
 Matches 67; Conservative 36; Mismatches 92; Indels 37; Gaps 11;
 QY 103 NMFREBPV--KKSIOSEAFPLDQSIPEERYKXKPLGICLID-----CTGN 148
 Db 14 NMFVETIGKSV--DSGIYLDSS-----YKMDYEMGICIIINNKPHKSTGMSSRGCT 67
 QY 149 EFTL--LRPTFSLGIVGVKFLHSMHGISOILGQFACKPEHRDVSVCYLVSQSGQS 206
 Db 68 DVANLRTFTFGLKQVKNKDLTREDLLEMDSVS--KEDSKSSSVCVILSHGDGV 126
 QY 207 VVGVDQTHSGPLPHIRFMFMGDCSPYLAGKPKMFIONVYVSDQLBDSILLEYDGPAM 266
 Db 127 IYV---TNGPVELKLTSTFRGDRYCRSLGRKPLFIQ---ACRTELDGQ--LETDGCT- 178
 QY 267 KNYEFAQKRGCLCTVREADFWSLCTADMSLLEQSHSPSYLQCSQKR 318
 Db 179 -DEWACQK-----IPVEDPLVAVSTAPGVYWSNKSXGDSWFIQSLCSMK 224
 RESULT 3
 ICE3_RAT STANDARD; PRT; 277 AA.
 AC PS5213; P70543; P97699; Q62933;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
 DE (SCA-1) (LICE) (IRP).
 OS CASP3 OR CPP32.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761236;
 RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
 RT a cysteine protease resembling interleukin-1 beta converting enzyme
 RT and CBD-3.";
 RL Oncogene 13:749-755 (1996).
 RN [2]
 RP SEQUENCE OF 30-241 FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=96042508; PubMed=7588240;
 RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,
 RA Hirstfield A.N., Tilly U.L.;
 RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and

```

FT CONFLICT 25 29 KSMDS -> QVD (IN REF. 4) .
FT CONFLICT 170 170 C-> S (IN REF. 2) .
FT CONFLICT 178 178 T-> A (IN REF. 2) .
FT CONFLICT 182 182 M-> V (IN REF. 2) .
FT CONFLICT 187 187 I-> K (IN REF. 2) .
FT CONFLICT 190 190 E-> G (IN REF. 2) .
FT CONFLICT 199 199 T-> S (IN REF. 3) .
FT CONFLICT 211 211 D-> G (IN REF. 2) .
FT CONFLICT 236 236 L-> I (IN REF. 4) .
FT CONFLICT 245 245 T-> M (IN REF. 3) .
SQ SEQUENCE 277 AA; 31491 MW; ADA8F418E2507402 CRC64;

Query Match 10.3%; Score 185.5; DB 1; Length 277;
Best Local Similarity 27.5%; Pred. No. 8,3je-07;
Matches 64; Conservative 37; Mismatches 93; Indels 39; Gaps 8;

QY 103 NNFRPEPKRS-IOESAPFLPQSLPERPKMSKPLGICLIID-----CIGNETE 151
Db 14 NNFEKTHGSKSMDSGLYDSS---YMDYPEKGLTIIINNNFKHSGMARNGTD 68
QY 152 L---LRDTFTSLGVEYQKFLHLSMAGISQLIGQFACMEPHRDYDFFVCVLVSRGSGSV 207
Db 69 VDAANLRRTFMALXVEVRANNNDLPRREIMELDMSVS-KEDHSKRSFVCVILSHGDEGI 127
QY 208 YGVDDTHSGFLPHIRRMFEGDSCPYLAGKPKKFFIQ-NIVVSGQLFEDSSLEVDGPA 265
Db 128 FG---TNPAPVDLKLTLTFPFPGDYCRSLTGPXKFLIIQACRGTELDGEGTSDGDDMAC 184
QY 266 MGNVFEKQKRGKGLCTVREHDFPMFSLCTADMSLLEQSHSPFLYQCHSOKLR 318
Db 185 QK-----IPEHDFLYASTARPGYMRNRSNDGSWFIQSLCAVLK 224

RESULT 4
ICE3 XENLA STANDARD; PRT; 282 AA.
ID ICE3 XENLA AC P5566;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptsin precursor [EC 3.4.22.-] (Cysteine protease CPP32) (CASP-3) (XCPP32) .
GN CASP3.
OS Xenopus laevis (African clawed frog) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
CC NCBI_Taxid=83355;
CC [1]_
CC SEQUENCE FROM N.A.
CC MEDLINE=97184166; PubMed=9030578;
CC Yaota Y., Nakajima K.;
CC "Induction of apoptosis and CPP32 expression by thyroid hormone in a
CC myoblastic cell line derived from tadpole tail.";
CC J. Biol. Chem. 272:5122-5127(1997) .
CC -1- FUNCTION: Important mediator of apoptosis. At the onset of
CC apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase
CC (PARP) at a 216-Asp-Gly-217 bond (By similarity).
CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12)
CC subunits.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity) .
CC -1- MISCELLANEOUS: The subunits are derived from the precursor
CC sequence by a probable autocatalytic mechanism and probably by
CC other caspases (By similarity) .
CC -1- SIMILARITY: Belongs to peptidase family C14.

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or send an email to license@isb-sib.ch) .

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CC EMBL: D89784; BAB14018.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILBCEZYME.
DR SMART; SMO0115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KM Hydroxylase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 186
FT CHAIN 187 282
FT ACT_SITE 131 174
FT ACT_SITE 174 174
SQ SEQUENCE 282 AA; 32124 MW; CB390E6980CAB77F CRC64;

Query Match 10.3%; Score 185.5; DB 1; Length 282;
Best Local Similarity 29.4%; Pred. No. 8.5e-07;
Matches 63; Conservative 33; Mismatches 71; Indels 47; Gaps 11;

128 ERYKMSKPLGICLID-----CIGNETEL-----LRDFTSLGYEV-----QKFLH 169
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
46 QNRTNYPENGLIINNKFHSNNANVCVDYALKHETFTGLGYEWVWCNDQK--- 102
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
170 LSWHGISQILGFACNPE--HRDYDFVCVLVSRGSGQ-SYGVQDQHSGLPLH--HRR 224
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
103 -----SSDITGLRLKISEEDHSKRSFVCAILSHGEDDSIGCV-----VPIHKNLTD 152
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
225 MFWGDSQPYLAGPKPKFTQNYVVSQGLDSSLLEVDENPAKNKEFFAKQKGLCTVARE 284
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
153 LFRDRKTLIVAKKFFIQ--ACRGTELDSC-IETDSCSEPREIQ-----RIVE 201
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
285 ADFEWSLCTADMSLLDQSHSSPSLYOCLSQKLR 318
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
202 ADFLYASTVPGYCSWRDKMDGSMFQLQSLCKMK 235
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
ICE3_CRILLO STANDARD; PRT; 277 AA.
AC 060431;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CpP-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-1).
GN CASP3 OR CPP32.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10030;
RX MEDLINE=96183165; PubMed=8605870;
RA Wang X., Zelenksi N.G., Yang J., Sakai J., Brown M.S.,
RA Goldstein J.L.;
RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
RT CPP32 during apoptosis."
EMBO J. 15:1012-1020(1996).
-f- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-

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CC helix leucine zipper domain and the membrane attachment domain.
CC cleaves and activates caspase-6, -7 and -9 (by similarity).
CC SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
CC (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC
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CC or send an email to license@sib-sib.ch).
CC
DR EMBL: U27463; AAB01511.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILBCEZYME.
DR SMART; SMO0115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KM Hydroxylase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9
FT CHAIN 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT_SITE 121 163
FT ACT_SITE 163 163
SQ SEQUENCE 277 AA; 31612 MW; 0BF3A4590A828A3 CRC64;

Query Match 10.2%; Score 183.5; DB 1; Length 277;
Best Local Similarity 27.9%; Pred. No. 1.2e-06;
Matches 67; Conservative 36; Mismatches 94; Indels 43; Gaps 9;

96 KSLKDPNNFRPEPVKKS-IQSEAFLLPOSIPERYKMKKPLGICLID----- 144
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
11 KSLK-----NPEVKTINGSKMSDGIYLDSS-----YKMDYPMGVCIILNNKPFKSTGM 61
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
145 --CIGNETEL--LRDFTSLGYEVQKFLHLSWHGISQILGFACNPEHRDYDFVCVLVS 200
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 TPRSGTDVPAAKLRETFMAKLYEVRKNDLTREELVELM-KVASKEDHSKRSFVCVILS 120
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
201 RGSQSYGVQDQHSGLPLHPIRMFMGDSCPYLAGKPKMFPIQ--NYVSDQGLDSSL 258
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 HDDEGVIFGID--GVIDLKULTYFRGDYCRSLGKPLFLIQACRGTELDGCIETDSG 177
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
259 LEVDGPKMKVPEFKQKRGCLTVHREADFFWGLCTADMSLLDQSHSSPSLYOCLSQKLR 318
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
178 TEDDMTCQK-----IPVEADFLVASTAPGYYSWRNPKDGSWFILQSLCMLK 224
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
ICE3_HUMAN STANDARD; PRT; 277 AA.
AC P42574; Q96AN1; Q96KP2;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CpP-32) (Caspase-3) (SREBP cleavage activity 1)

```

DE (SCA-1).
GN CASP3 OR CPP32.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RC TISSUE=T-cell;
RX MEDLINE=95074098; PubMed=7983002;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT CPP32, a novel human apoptotic protein with homology to
RT Caenorhabditis elegans cell death protein Ced-3 and mammalian
RT Interleukin-1 beta-converting enzyme.";
RL J. Biol. Chem. 269:30761-30764 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnecers S., Zeng Z.,
RA Beutler D.R., Poitrier G.G., Salvesen G.S., Dixit V.M.;
RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809 (1995).
RN [3]
RP SEQUENCE FROM N.A.
RA Vallette F.M., Oliver L.J.;
RT "Control of the activation of the procaspase-3 by a sequence located
RT at the N-terminus of the p17 subunit.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-N.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Strusberg R.J., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman A., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzyzanski M.I., Skalka U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903 (2002).
RN [6]
RP SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.
RX MEDLINE=95319529; PubMed=7596430;
RA Nicholson D.W., Ali A., Thornberry N.A., Viallancoeur J.P., Ding C.K.,
RA Gallant M., Gareau Y., Griffitt P.R., Labelle M., Lazebnik Y.A.,
RA Munday N.A., Raju S.W., Smulson M.E., Yamin T.-T., Li V.L.,
RA Miller D.K.;
RT "Identification and inhibition of the ICE/CED-3 protease necessary
RT for mammalian apoptosis.";
RL Nature 376:37-43 (1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
RX MEDLINE=96266352; PubMed=8673606;
RA Rotonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Viallancoeur J.P.,
RA Thornberry N.A., Becker J.W.;
RT "The three-dimensional structure of apopain/CPP32, a key mediator of
RT apoptosis.";
RL Nat. Struct. Biol. 3:619-625 (1996).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
RX MEDLINE=97197830; PubMed=9045680;
RA Mitzi P.R.E., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
RA Wittel J.P., Tomaselli K.U., Grueter M.G.;
RT "Structure of recombinant human CPP32 in complex with the
RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
RL J. Biol. Chem. 272:6539-6547 (1997).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=20283632; PubMed=10621855;
RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
RA Levy M.A., Dewolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
RA Ryan M.D., Haltiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
RA Lark M.W., Nadeau D.P., Suva L.J., Goven M., Nuttall M.E.;
RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
RT inhibit apoptosis and maintain cell functionality.";
RL J. Biol. Chem. 275:16007-16014 (2000).
RN [10]
RP PROCESSING.
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Tripani A.A., Tomaselli K.U.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469 (1996).
RN [11]
RP CLEAVAGE OF HUNTINGTIN.
RX MEDLINE=96331285; PubMed=8696339;
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
RA Viallancoeur J.P., Hayden M.R.;
RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
RT is modulated by the polyglutamine tract.";
RL Nat. Genet. 13:442-449 (1996).
RN [12]
RP FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-|-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9. Involved in the
CC cleavage of huntingtin.
CC -1- ENZYME REGULATION: Inhibited by isatin sulfonamides.
CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
CC and kidney. Moderate levels in brain and skeletal muscle, and low
CC in testis. Also found in many cell lines, highest expression in
CC cells of the immune system.
CC -1- PFM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
CC AND VICE VERSA.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC EMBL: U13737; AAA65015.1; -.
DR EMBL: U13738; AAB60355.1; -.
DR EMBL: U26943; AAA74929.1; -.
DR EMBL: A041369; CAC08866.1; -.
DR EMBL: A219866; AAO25654.1; -.
DR EMBL: BC016926; AAI16926.1; -.
DR PIR: A55315; A55315.
DR PDB: 1PAU; 07-JUL-97.
DR PDB: 1CP3; 24-DEC-97.
DR PDB: 1GRW; 23-JUN-00.
DR MEROPS; C14.003; -.
DR Genew; HGNC:1504; CASP3.
DR MIM; 600636; -.
DR GO; GO:0004208; F:caspase-3 activity; TAS.
DR GO; GO:0008624; P:induction of apoptosis by extracellular sig. .; TAS.
DR GO; GO:0008629; P:induction of apoptosis by intracellular sig. .; TAS.
DR GO; GO:0009405; P:apoptogenesis; TAS.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PRO0376; IL1BCENZME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KM Hydroclase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
KM 3D-structure.
FT PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175 ADOPAIN P17 SUBUNIT.
FT CHAIN 176 277 ADOPAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT VARIANT 190 190 D -> E (in isoform beta).
/FTID-VAR 001401.
CONFLECT 31 36
STRAND 36 36 ISDMS -> MSWDTG (IN REF. 3).
STRAND 43 51
HELIIX 57 59
TURN 60 60
TURN 65 66
TURN 67 80
HELIIX 81 82
TURN 81 82

Query Match 10.2%; Score 183.5; DB 1; Length 277;
Best Local Similarity 26.4%; Pred. No. 1.2e-06;
Matches 64; Conservative 41; Mismatches 100; Indels 37; Gaps 7;

OY 98 LKDSNNPREPVK---KIQSEARLPQSIPEERYKKSKPLGLGICLIID----- 144
DB 1 MENTENSVDKSKIKNLEPKIITHGSESDSGISLDNRYKNDYPMKGLCIITNNKPHKSTG 60
OY 145 ---CIGNETEL--LRDTFTSLGYEVQKFLHLSMHGISQILGAPACMPREEDYDFFVCILV 199
DB 61 MTSRSGTVDVDAANREPRRLKLYEVKKNDLTREELVEIMLRDVS-XEDSKSSSFYCVLL 119
OY 200 SRGSGQSYGYVDQHGSGPLPHIRFMWGDSCTPLAKRKPQFTIO--NYVSDGQLEDS 257
DB 120 SHGEGGIIFG---TNGPVDLKRITNFRGDRCSLTGKPKLFTIIQACRGTELDGIEITDS 176
OY 258 LLEVDPAMKRVFPAKQKGLCTVHRADPFWSLCTADMSLILQSHSSPSLYLQCLSQL 317
DB 177 GYDDDMACHK-----IPVDADFLVAVSTAPGYVSRNNSMDGSMFQSLCAWL 223
OY 318 RQ 319
DB 224 KQ 225

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RESULT 7
ICE6 MOUSE STANDARD; PRT; 276 AA.
ID ICE6 MOUSE
AC 008738;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
GN Caspe.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen W., Vandenaebroeck P., Declercq W., van den Brande I.,
RA van Lee G., Moelans F., Schotte P., van Crielinge W., Beyaert R.,
RA Piers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves poly(ADP-ribose)
CC polymerase in vitro, as well as lamins. Overexpression promotes
CC programmed cell death (By similarity).
CC -1- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Highly expressed in lung, liver, kidney,
CC testis, and heart. Lower levels in spleen, skeletal muscle and
CC brain.
CC -1- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
CC SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y13087; CAA73529.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.005; -.
DR MCD; MGI:1312921; Casp6.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001308; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PRO0376; IL1BCENZME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KM Hydroclase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 5
FT CHAIN 6 162 CASPASE-6 SUBUNIT P18 (BY SIMILARITY).
FT PROPEP 163 176 BY SIMILARITY.
FT CHAIN 177 276 CASPASE-6 SUBUNIT P11 (BY SIMILARITY).
FT ACT_SITE 104 104 BY SIMILARITY.
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 276 AA; 31595 MW; 5965DE9321126B6C CRC64;

Query Match 9.6%; Score 172.5; DB 1; Length 276;
Best Local Similarity 27.8%; Pred. No. 7.7e-06;
Matches 62; Conservative 26; Mismatches 84; Indels 51; Gaps 8;

OY 126 PEERYKKSKPLGLGICLIID-----CIGNETELLRDTFTSLGYEVQK----- 167

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Db 16 PAEQYMDHRRGVALIFNHERFWHLTPERRGTNADRDNLTRFSDLGFEVCKFNDLR 75
 Qy 168 ---LHLSMGIISQIGQFACMEHEDYDSFVCLVSRGSGSYGV-----CHSGTLP 219
 Db 76 AEBLLKIHVE-----TSHIDACDFICVFSHGBGNVAYPAKIEIQTITGL-- 125
 Qy 220 HHIREFMWDCSPYLAGKPKMFQIONVYVSDGQEDSSILEVD-----GPAMKVEFKAQ 274
 Db 126 -----FKGDKCQSQVXKXPIFIQ---ACRGSGHDPVVPVLDWVDHDTKDVT--QVD 175
 Qy 275 KXGLCTVREADFPFWSLCTADWSLLEQSHSPSLYLOCTSKL 317
 Db 176 AASVTLPAGADFLMCIYASGYSYSHRTVNGSMYIDLCBML 218

RESULT 8
 ICE7 HUMAN STANDARD: PRT: 303 AA.
 AC P55210: Q13364: Q96B80;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
 DE (ICE-LAP3) (Apoptotic protease Mch-3) (CMT-1).
 GN CASP7 OR MCH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=96139498; PubMed=8576161.
 RA Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
 Dixit V.M.,
 RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
 cell death protein Ced-3 is activated during Fas- and tumor necrosis
 factor-induced apoptosis.";
 RL J. Biol. Chem. 271:1621-1625(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX TISSUE=Spleen;
 RX MEDLINE=96147144; PubMed=8567622;
 RA Lipkne J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;
 RT "Identification and characterization of CPP32/Mch2 homolog 1, a novel
 cysteine protease similar to CPP32.";
 RL J. Biol. Chem. 271:1825-1828(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RX TISSUE=T-cell;
 RX MEDLINE=96105019; PubMed=8523391;
 RA Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,
 Fritz L.C., Tomaselli K.J., Wang L., Yu Z., Croce C.M., Salvenson G.,
 Barnshaw W.C., Litwack G., Alnemri E.S.,
 RT "Mch3, a novel human apoptotic cysteine protease highly related to
 CPP32.";
 RL Cancer Res. 55:6045-6052(1995).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND ALPHA').
 RX TISSUE=Fetal lung, and Fetal spleen;
 RX MEDLINE=97224489; PubMed=9070923;
 RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 Copeland N.G., Fletcher P.A.,
 RT "Identification and mapping of Casp7, a cysteine protease resembling
 CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
 RL Genomics 40:86-93(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX TISSUE=Skin;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Bromberg M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP PROCESSING.
 RX MEDLINE=96353838; PubMed=8755496;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasan S.M.,
 Wang L., Bultrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 apoptotic cysteine protease containing two FADD-like domains";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 responsible for apoptosis execution. Cleaves and activates sterol
 regulatory element binding proteins (SREBPs). Proteolytically
 cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217
 bond. Overexpression promotes programmed cell death.
 CC -1- ENZYME REGULATION: Inhibited by Icatin sulfonamides.
 CC -1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=Alpha;
 CC IsoId=P55210-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=P55210-2; Sequence=VSP_000807;
 CC Note=Not proteolytically active;
 CC Name=Alpha'; Synonyms=Beta;
 CC IsoId=P55210-3; Sequence=VSP_000806;
 CC Note=What we call isoform Alpha' is known in Ref.4 as Beta;
 CC -1- TISSUE SPECIFICITY: Highly expressed in lung, skeletal muscle,
 CC liver, kidney, spleen and heart, and moderately in testis. No
 CC expression in the brain.
 CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 CC VICE VERSA.
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: U39613; AAC50346.1; -
 CC EMBL: U40281; AAC50352.1; -
 CC EMBL: U37448; AAC50303.1; -
 CC EMBL: U37449; AAC50304.1; -
 CC EMBL: U67319; AAC51152.1; -
 CC EMBL: U67320; AAC51153.1; -
 CC EMBL: U67206; AAF21460.1; -
 CC EMBL: BC015799; AAF15799.1; -
 CC PDB: 1FIJ; 23-MAY-01.
 CC PDB: 1IGF; 04-JAN-02.
 CC PDB: 114O; 31-OCT-01.
 CC PDB: 1151; 23-FEB-02.


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FT DOMAIN <1 55 CARD.
FT ACT_SITE 210 BY SIMILARITY.
FT ACT_SITE 253 BY SIMILARITY.
FT NON_TER 312
SQ SEQUENCE 312 AA; 35070 MW; 318A0746212B5646 CRC64;

Query Match 9.3%; Score 167.5; DB 1; Length 312;
Best Local Similarity 31.1%; Pred. No. 2.1e-05;
Matches 46; Conservative 22; Mismatches 61; Indels 19; Gaps 4;

QY 130 YMKSKPGICILIDCI-----GNBTE--ILRDTFSLGVEYCKFLHSMHG1 175
DB 125 YRQSPRLALVMSNVHFTGKDLFRSGGDVHTTLVTLFKLGYNVHLYDQIAQEM 184
QY 176 SOLGQFACMPHPRDYDSFVCLVSRGSGSVGVQDTHSGLPHTIRPMGSDCPYLA 235
DB 185 GELQNFAGLPAHRTVDSQIVALLSHGVGGIYGV--GKLLQGVFRLEPDNANCPSLQ 242
QY 236 GPKKPFITQNVVSGQLBDSLEVDG 263
DB 243 NKPKMFFIQ--ACRGDETRGVDDQDG 267

RESULT 10
ICE7 MOUSE STANDARD; PRT; 303 AA.
AC P97864; 008669;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE2 cysteine protease) (Apoptotic
  protease Mch-3).
GN Casp7 OR MCH3 OR LICE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argente J.M., Jenkins N.A., Gilbert D.J.,
RT "Identification and mapping of Casp7, a cysteine protease resembling
  CPB32 beta, interleukin-1 beta converting enzyme, and CED-3.",
RL Genomics 40:86-93(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; PubMed=9125129;
RA Mukasa T., Khoroqui Y., Tsukahara T., Momoi M.Y., Kimura I.,
RT "Mortamun enhances CPB32-like activity during neuronal
  differentiation of P19 embryonal carcinoma cells induced by retinoic
  acid.",
RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaesbeek P., Declercq W., van den Brande I.,
RA van Looy G., Molemans F., Schotte P., van Clijckinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dalceneno L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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Db      6 DCAAELEKVDSSSEDDVDKAPDRSSSTISSILLKKK----- 40
Qy      97 SLKPSNNREEPYKKSIOESEAFLPQSIPEERYKMKSPGLICLITD-----CI 146
Db      41 -----RMSAGVFRGT-----RDRVPTLYLRNDPQMKKCIINNNKPKATGADV 86
Qy      147 GNETE-----LLADTFSLGVEYVKFLHLSMHGISQLLGQFACMPHRYDSEFVCVYLRG 202
Db      87 RNTGTDADAGLFFCFQNLGFVYVHNHDCSCAKMDLLRK-ASEEDHNSACFACVLSHG 145
Qy      203 GSGSYVGVDPDTHSGPLHRIIRFMWGDSCPYLAGKPKFFIYVSDGLQEDSSLEFVD 262
Db      146 EEDLYGKDGVV--TPIKDLTAHFRDGRCKTLLEKXLFPII--ACRGTELDG--IQAD 198
Qy      263 GPMKRVKVEFAKRGGLCTVAREDFWMSLCTADMSLLEQSHSPSLYLQCSQKLRQ 319
Db      199 SGPTINDIDANPRNK---IPVEADFLFAYSTVPGYISWNPGRKGSWFVALCSITLNE 251

RESULT 11
ICE7_MESAU STANDARD; PRT; 303 AA.
AC      P55214;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
DE      (ICE-LAP3) (Apoptotic protease Mch-3) (SRBP cleavage activity 2)
DE      (SCA-2).
DN      CASP7 OR MCH3.
OS      Mesocricetus auratus (Golden hamster).
OS      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC      Mesocricetus.
OX      NCBI_TaxID=10036;
RN      [1]
RP      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX      STRAIN=Syrian; TISSUE=Liver;
RX      MEDLINE=96224303; PubMed=8643593;
RA      Pal J.-T., Brown M.S., Goldstein J.L.;
RA      "Purification and cDNA cloning of a second apoptosis-related cysteine
RT      protease that cleaves and activates sterol regulatory element binding
RT      proteins."; Acad. Sci. U.S.A. 93:5437-5442(1996).
RL      Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
CC      -1- FUNCTION: Involved in the activation cascade of caspases
CC      responsible for apoptosis execution. Cleaves and activates sterol
CC      regulatory element binding proteins (SRBPs). Proteolytically
CC      cleaves poly(ADP-ribose) polymerase (PARP) at a 216-ASP-Gly-217
CC      bond. Overexpression promotes programmed cell death (by
CC      simlarity).
CC      -1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
CC      (by simlarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- PTM: CLEAVAGES BY GRAZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC      SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC      CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC      CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC      VICE VERSA (BY SIMILARITY).
CC      -1- SIMILARITY: Belongs to peptidase family C14.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U47332; AAC52595.1; -.
DR      HSSB; P42574; 1PNU.
DR      MEROPS; C14.004; -.
DR      InterPro; IPR002138; ICE_p10.
DR      InterPro; IPR001309; ICE_p20.

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DR      InterPro; IPR002398; Peptidase_C14.
DR      Pfam; PR00656; Peptidase_C14; 1.
DR      PRINTS; PR00376; ILIBENZYM.
DR      SMART; SM00115; CASc_1.
DR      PROSITE; PS01122; CASPASE_CYS_1.
DR      PROSITE; PS01121; CASPASE_HIS_1.
DR      PROSITE; PS50207; CASPASE_P10; 1.
DR      PROSITE; PS50208; CASPASE_P20; 1.
KW      Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT      PROPEP      1      23
FT      CHAIN      24      198
FT      PROPEP      199      206
FT      CHAIN      207      303
FT      ACT_SITE      144      144
FT      ACT_SITE      186      186
SQ      SEQUENCE      303 AA; 34037 MW; EA29356D90984648 CRC64;

Query Match      9.0%; Score 162.5; DB 1; Length 303;
Best Local Similarity 26.9%; Pred. No. 4,9e-05;
Matches 58; Conservative 31; Mismatches 92; Indels 35; Gaps 8;

Qy      125 IPERYKMKSKPLIGLICIT-----DCIGNETELLRDTFTSLGVEYVKFLHL 170
Db      55 VPTLYLRMDFEKMKKCIINNNKPNFKYGMVNRNGTDAEALFKCFRSLGPDVYVYND 114
Qy      171 SMHGISQLLGQFACMPHERHDYDSFVCVLYSRGSGSYVGVDPDTHSGPLHRIIRFMWGD 230
Db      115 SCAMQDMLRK-ASEEDHNSACFACVLSHGENTLIYKQGV--TPIKDLTAHFRDR 170
Qy      231 CPYLAKPKMFFIQ--NVVSDG-QLEDSSLEVDGPMKRVKFAKRGGLCTVHRAD 286
Db      171 CKTLRKPLKFLFIQACRGTELDGVQADSGPINETDA-----NPRK-----IPVEAD 218
Qy      287 FFWSLCTADMSLLEQSHSPSLYLQCSQKLRQERG 322
Db      219 FLFAYSTVPGYISWNPGRKGSWFVALCSITL-DEHG 253

RESULT 12
ICE1_DROME STANDARD; PRT; 323 AA.
AC      002032; Q9WIN0;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Caspase-1 precursor (EC 3.4.22.-).
DN      DCP-1 OR CG5370.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A., AND SEQUENCE OF 216-248.
RX      TISSUE=Embryo;
RX      MEDLINE=20196006; PubMed=8999799;
RA      Song Z., McCall K., Steller H.;
RA      "DCP-1, a Drosophila cell death protease essential for development.";
RT      Science 275:536-540(1997).
RL      Science 275:536-540(1997).
RN      [2]
RP      ERRATUM.
RA      Song Z., McCall K., Steller H.;
RL      Science 277:167-167(1997).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      STRAIN=Berkley;
RX      MEDLINE=10731132;
RA      Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA      Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA      George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA      Sutton G.G., Wortman J.R., Vandal M.D., Zhang O., Chen L.X.,
RA      Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
RA      Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

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RA Abril J.F., Appayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Bouchan M.R., Bouck U., Brokstein P., Brothier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Evans G., Ferraz C., Ferrera S., Fleschmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fierstra S., Glasser K.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Godek A., Gong F., Gorrell U.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison U.A., Ketchum K.A.,
RA Kimmel B.E., Kodra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milstina N.V., Mobarry C., Morris J., Moshireit A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spiedling A.C., Stapleton M., Strong R., Sun E.,
RA Svitkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster.",
RL Science 287:2185-2195(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; TISSUE=Embryo;
RA Stapleton M., Brokstein P., Hong L., Appayani A., Carlson J.W.,
RA Chape M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Krommiller B., Li P.W., Liao G.,
RA Matela A., Mungali C.J., Nuno J., Paclebo J.M., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.E.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution (By similarity).
CC Proteolytically cleaves poly(ADP-ribose) polymerase (PARP). Loss
CC of zygotic DCP-1 function causes larval lethality and melanotic
CC tumors.
CC -1- SUBUNIT: Heterodimer of a 22 kDa (p22) and a 13 kDa (p13) subunit.
CC -1- DEVELOPMENTAL STAGE: Present uniformly throughout embryos of
CC stages 4 and 10. In stage 16 embryos, the expression becomes
CC restricted to the central nervous system, the developing gonads,
CC and a portion of the gut. In stage 17 embryos, expression is
CC mainly localized in cells along the midline of the central nervous
CC system.
CC -1- SIMILARITY: Belongs to peptidase family C14.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF001464; AAB58237.1; -
CC EMBL: AE003461; AAF47027.1; -
CC EMBL: BT010065; AAQ2534.1; -
CC HSSP: P42574; IPAU.
CC MEROPS: C14.016; -
CC PDBase: FBgn0010501; DCP-1.
CC GO: GO:0004159; F:effector caspase activity; IDA.
CC GO: GO:0004207; F:effector caspase activity; NAS.
CC GO: GO:003036; P:actin cytoskeleton organization and biogenesis; IMP.

DR GO: GO:000632; P:apoptotic program; IDA.
DR GO: GO:0006922; P:cleavage of lamin; IMP.
DR GO: GO:000795; P:embryonic morphogenesis; IMP.
DR GO: GO:0007300; P:nurse cell/ocyte transport (sensu insecta); IMP.
DR InterPro: IPR002138; ICE p10.
DR InterPro: IPR001309; ICE p20.
DR InterPro: IPR002398; Peptidase C14.
DR Pfam: PF00655; Peptidase C14; I.
DR PRINTS: PR00376; ILICBNZTME.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS0207; CASPASE_P10; 1.
DR PROSITE: PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 33 PROBABLE.
FT CHAIN 34 202 CASPASE-1 SUBUNIT P22.
FT PROPEP 203 215
FT CHAIN 216 323 CASPASE-1 SUBUNIT P13.
FT ACT_SITE 154 154 BY SIMILARITY.
FT ACT_SITE 196 196 BY SIMILARITY.
SQ SEQUENCE 323 AA; 3592 MW; B5F0F75E8E2BD CRC64;

Query Match 8.3%; Score 150; DB 1; Length 323;
Best Local Similarity 25.2%; Pred. No. 0.00045;
Matches 59; Conservative 37; Mismatches 94; Indels 44; Gaps 9;

OY 101 PNNNF-REEVKKSIDSESEFLPQSIPEERYMKSKPGICLI-----IDCIGNET-- 150
DB 54 PANKFVAKMFEVRYASB-----YNNSHKGRVALIFNHEFFDIPSLKSRGT 100
OY 151 ----ELRDRFTSLGYEVQKFLALSMHGISQILGCFACPEHRDYDSFVCLVSRGQS 206
DB 101 NVDAQELKKAFFNLGFAVSVHKCKRLDILKVVKAEL-DRTDNDCLAVAILSHGNGY 159
OY 207 VYGVDCQHSPLPHHRRNFMGSCPYLAGKRMPT--QYVVSQQLSESSLLRYDG 263
DB 160 LVAKDQYK--LDNIWHYFTATPCPSLGRKRLFFIQACQDRLDGGITTEKGVETDG 216
OY 264 PANKVVEFKQKRGCLCTVHREADFFWSLCTADMSLLEGSSPSLYLOCSQL 317
DB 217 ESSISYKLT-----PIH--ADFLFSYSTIGGYFSKNNKNGSVYMSGLREL 260

RESULT 13
ID ICE DROME STANDARD; PRT; 339 AA.
AC 001382; Q9VAH1;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase precursor (EC 3.4.22.-) (dtcB).
GN ICB OR CG7788.
OS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
CC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97327558; PubMed=9184225;
RA Fraser A.G., Evan G.I.;
RT "Identification of a Drosophila melanogaster ICE/CED-3-related
RT protease, dtcB.",
RL EMBL J. 16:2805-2813(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Maniatis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner K., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abiri J.F., Abhyani A., An H.-J., Andrews-Piankoff C., Baldwin D.,
 RA Baller R.M., Banu A., Bakendale U., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.D., Benos F.V., Bernan B.P., Bhattacharya D., Boltovskoy S.,
 RA Botkova D., Botchan M.R., Bouck J., Brockstein P., Bottlier P.,
 RA Butts K.C., Buam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielsen A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodex A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 RA Hovatt N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Houten D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kension J.A., Ketchum K.A.,
 RA Kimball B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobery C., Morris J., Moshirei A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murty D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
 RA Palazzolo K., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan N., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zheng F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 RN [3].
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkely; TISSUE=Head;
 RC MEDLINE=22425066; PubMed=12537569;
 RX Stapleton M., Carlson J.W., Brockstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Krommiller B., Paclebo J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A Drosophila full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 responsible for apoptosis execution. Acts downstream of rpr.
 CC Cleaves baculovirus p35 and Iamun DMO in vitro.
 CC -!- SUBUNIT: Heterodimer of a 21 kDa (p21) and a 12 kDa (p12) subunit.
 CC -!- DEVELOPMENTAL STAGE: Expressed at all stages where apoptosis
 occurs.
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Y12261; CAA72937.1; -;
 DR EMBL: AE003771; AAF56939.1; -;
 DR EMBL: AY058451; AAF13680.1; -;
 DR HSSP: P42574; 1PAU.
 DR MEROPS: C14.015; -;
 DR FLYBASE: FBgn0019972; Ice.
 DR GO: GO:0004207; P:effector caspase activity; NAS.
 DR GO: GO:0006915; P:apoptosis; NAS.
 DR InterPro: IPR001309; ICE_p10.
 DR InterPro: IPR002398; Peptidase C14.
 DR Pfam: PF00656; Peptidase C14; I.
 DR PRINTS: PR00376; ILBCNZME.

DR SMART: SM00115; CASc; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PSS0207; CASPASE_P10; 1.
 DR PROSITE: PSS0208; CASPASE_P20; 1.
 DR PROSITE: PSS0209; CASPASE_P20; 1.
 DR HYDROLASE; Thiol protease; Zymogen, Apoptosis.
 FT PROPEP 1 28
 FT CHAIN 29 217
 FT PROPEP 218 230
 FT CHAIN 231 339
 FT ACT_SITE 169 169
 FT ACT_SITE 211 211
 FT ACT_SITE 211 211
 FT CONFLICT 151 151
 FT CONFLICT 265 265
 SQ SEQUENCE 339 AA; 37363 MW; E105ED29518507EC CRC64;
 Query March 8.3%; Score 149.5; DB 1; Length 339;
 Best Local Similarity 24.2%; Pred. No. 0.00052;
 Matches 63; Conservative 40; Mismatches 108; Indels 49; Gaps 11;
 79 VQAGTGYRNVLCMAIQKSLKDPNNFRPEPKSIQSEAEFLPOSIPERYKMSKPLG 138
 44 VAGSSHYGSGAIGQANGYSSPSRYKN-VAKQVTDRA-----AEYMHKXRG 94
 139 ICIL-----IDCGNETLRLDPTFSLGYNQKFLHSMHGISQLG 180
 95 MALIFNHEHEVPTLKRAGTNDVDC-ENLTVLK---QLDEVTVYKDCRYKDLRLT- 148
 181 QPACMEBHRDYDSFVCULSRGSGGVYGVDPQTHSGPLPHIRRPMPGDCPYLAGKPKM 240
 149 EYASQNHSSDIDLVAISHGEMGYIVAKDQYK--LDNWSFTFNHHCSSLGKPKRL 205
 241 PFT---QNVYSSGQLDEBSLLEVDGPAMKNVEFKAQKGLCTVHREADPMSLTADWS 297
 206 FFLQACQGRDLGGVGMQSRQETEDGDS--SMSYK-----IPVH-ADFLVAVSTVDFG 255
 298 LLEQSHSPSLYQCLSOYK 317
 256 YSRNRTTRGSMQSLCAEL 275
 RESULT 14
 ID_CEL_SPOFR STANDARD; PRT; 299 AA.
 AC P891G;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-1 precursor (EC 3.4.22.-).
 OS Spodoptera frugiperda (Fall armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Noctuidae; Amphipyritinae; Spodoptera.
 CX NCBI_taxid=7108;
 RN [1]
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=97151084; PubMed=8999805;
 RA Ahmad M., Srinivasula S.M., Wang L., Litwack G., Fernandes-Alnemri T.,
 RA Alnemri E.S.;
 RT "Spodoptera frugiperda caspase-1, a novel insect death protease that
 RT cleaves the nuclear immunophilin FKBP46, is the target of the
 RT baculovirus antiapoptotic protein p35.";
 RL J. Biol. Chem. 272:1421-1424(1997).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 responsible for apoptosis execution (By similarity). Inhibited by
 CC the baculovirus anti-apoptotic protein p35. Cleaves p35 and
 CC nuclear immunophilin FKBP46.
 CC -!- SUBUNIT: Heterodimer of a 19/18 kDa (p19/18) and a 12 kDa (p12)
 CC subunit.
 CC -!- SUBUNIT: AN AUTOCATALYTIC MECHANISM GENERATES THE TWO ACTIVE SUBUNITS.
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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CC EMBL; U81510; AAC7442.1; -
 DR HSSP; P42574; 1CP3.
 DR MEROPS; C14.015; -
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; 1LBCENZYM.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KM Hydrolyase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 28
 FT CHAIN 29 184 CASPASE-1 SUBUNIT P19/18.
 FT PROPEP 185 195 POTENTIAL.
 FT CHAIN 196 299 CASPASE-1 SUBUNIT P12.
 FT ACT_SITE 136 136 BY SIMILARITY.
 FT ACT_SITE 178 178 BY SIMILARITY.
 SQ SEQUENCE 299 AA; 33527 MW; 99F4FED09B04EEDE CRC64;

Query Match 7.9%; Score 142.5; DB 1; Length 299;
 Best Local Similarity 24.1%; Pred. No. 0.0015;
 Matches 66; Conservative 37; Mismatches 112; Indels 59; Gaps 12;

QY 62 NHRDLKTKIQKQVQAGTSRVNLQALIKSLKDSNNFRPREPKYSQSEEARL 121
 DB 10 NVDSDYDI-----KQRTNGGGDE-----GDALGSSSSQPNVARKPVDNR----- 49
 QY 122 PQSIEPERYKMKSKFLGICLI-----IDCIGNET-----ELLRDTFSLGEYQKFL 168
 DB 50 -----APYNNMNHKRGKALIFNNEHDPHSLKRTGTNVDSNLKVLKLGKVTVP 104
 QY 169 HLSMHGIGSQILGQFACMPERHDYSPVCVLVSRGSGSVYGVQDTHSGCLPHHIRMFMG 228
 DB 105 NIKSEINKFLIQQTAEK-DHSDDADCLVAVALTHGELMLYAKD-TH--YKPDWLWYFYRA 160
 QY 222 DSCPTLAGKPKMFQONVYVSDGQLEDS-----SLLEVDPAMKVEFKAKQKGLCTVHRE 284
 DB 161 DKCPTLAGKPKLFFIQ--ACQSPRLDGGITLSTETDSSPSYSYR-----FVH-- 207
 QY 285 ADFWSLCTADMSILBOGSHSSPSLYLQCLGKLR 318
 DB 208 ADFLIASFVPGYFSEMTTRGSMFMQLCELR 241

RESULT 15
 CFWA_MCV1 STANDARD; PRT; 241 AA.
 AC Q98325; O11298;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Viral CASPs and FADD-like apoptosis regulator (v-CFLAR) (Viral
 DE FLICE-inhibitory protein) (v-FLIP).
 GN 159L OR H-H2.2.
 OS Moluscum contagiosum virus subtype 1 (MCV1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Moluscipoxvirus.
 OX NCBI_TaxID=10280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96325459; PubMed=8670425;
 RA Senkevich T.G., Bugert U.J., Sisler U.R., Koonin E.V., Darai G.,
 RA Moss B.;

RT "Genome sequence of a human tumorigenic poxvirus: prediction of
 RT specific host response-evasion genes.";
 RL Science 273:813-816(1996).
 RN [2]
 RN SEQUENCE OF 91-241 FROM N.A.
 RX MEDLINE=97352177; PubMed=9208457;
 RA Moratilla M., Agronoy M., Nunez A., Funes J.M., Varas A.J.,
 RA Lopez-Estebaran U.L., Estebar M., Martin-Gallardo A.,
 RT A random DNA sequencing, computer-based approach for the generation
 RT of a gene map of moluscum contagiosum virus.";
 RL Nature Genes 14:73-80(1997).
 RN [3]
 RN FUNCTION.
 RP MEDLINE=97242415; PubMed=9087414;
 RX Thome M., Schneider P., Hofmann K., Fickenscher H., Meini E.,
 RA Neipel F., Matmann C., Burns K., Bodmer U.L., Schroeter M.,
 RA Scalfidi C., Krammer P.H., Peter M.E., Tschopp U.;
 RT "Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced by
 RT death receptors.";
 RL Nature 386:517-521(1997).
 RN [4]
 RN FUNCTION.
 RP MEDLINE=97188440; PubMed=9037025;
 RX Bertin J., Armstrong R.C., Oltine S., Martin D.A., Wang Y., Banks S.,
 RA Wang G.-H., Senkevich T.G., Alnemri E.S., Moss B., Lenardo M.J.,
 RA Tomaselli K.J., Cohen J.I.;
 RT "Death effector domain-containing herpesvirus and poxvirus proteins
 RT inhibit both Fas- and TNFR1-induced apoptosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:1172-1176(1997).
 RN [5]
 RN CHARACTERIZATION.
 RP MEDLINE=99457304; PubMed=10526240;
 RX Tsukumo S.I., Yonehara S.;
 RA "Requirement of cooperative functions of two repeated death effector
 RT domains in caspase-8 and in MCL15 for induction and inhibition of
 RT apoptosis, respectively.";
 RL Genes Cells 4:541-549(1999).

CC -1- FUNCTION: INHIBITS TNFRSF1A, TNFRSF6 AND TNFRSF12 INDUCED
 CC APOPTOSIS. MAY INTERFERE WITH CASPASE-8 RECRUITMENT AND ACTIVATION
 CC AT THE DEATH-INDUCING SIGNALING COMPLEX (DISC). MAY LEAD TO HIGHER
 CC VIRUS PRODUCTION AND CONTRIBUTE TO VIRUS PERSISTENCE AND
 CC ONCOGENICITY.
 CC -1- SUBUNIT: ASSOCIATES WITH THE DEATH-INDUCING SIGNALING COMPLEX
 CC (DISC) FORMED BY TNFRSF6, FADD AND CASPASE-8. INTERACTS WITH FADD.
 CC -1- SIMILARITY: Contains 2 death effector (DED) domains.
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CC EMBL; U60315; AAC55287.1; -
 DR EMBL; U86888; AAB57923.1; -
 DR PIR; T30761; T30761.
 DR InterPro; IPR001875; DED.
 DR Pfam; PF01335; DED; 2.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PS50168; DED; 2.
 KW Apoptosis; Repeat.
 FT DOMAIN 8 78 DED 1.
 FT DOMAIN 95 175 DED 2.
 SQ SEQUENCE 241 AA; 26939 MW; 135C9F80B369E216 CRC64;

Query Match 6.8%; Score 122; DB 1; Length 241;
 Best Local Similarity 25.3%; Pred. No. 0.038;
 Matches 37; Conservative 31; Mismatches 48; Indels 30; Gaps 5;

QY 1 MAEIGEDLDKSDVSSL-IFL--MKDYMGKSKSKESFDDLYVELEKLNVAAPDDLDLE 57
 DB 100 MCVGEIDLSSELRALRLFACNLNPSLSTA-LSSESRFVELVALENGLVSPSSSVYLA 158

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:52:33 ; Search time 118 Seconds

(without alignments)
930.511 Million cell updates/sec

Title: US-10-713-208-6

Perfect score: 1800
Sequence: 1 MARIGEDLPKSDVSLIFLM.....ITKSKMHFSSIGLILDLVL 348

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 700785

Minimum DB seq length: 0

Maximum DB seq length: 348

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 345 | 15.2 | 218 | 11 Q99MZ5 | Q99MZ5 ratius norv |
| 2 | 277 | 15.4 | 78 | 6 Q8MJ18 | Q8MJ18 macaca mla |
| 3 | 214 | 11.9 | 283 | 13 Q93417 | Q93417 gallus gall |
| 4 | 199 | 11.1 | 303 | 13 Q91B65 | Q91B65 xenopus lae |
| 5 | 193.5 | 10.8 | 277 | 6 Q95ND5 | Q95ND5 sus scrofa |
| 6 | 192.5 | 10.7 | 318 | 13 Q91B65 | Q91B65 xenopus lae |
| 7 | 192 | 10.7 | 277 | 6 Q8MK15 | Q8MK15 canis famli |
| 8 | 190.5 | 10.6 | 313 | 11 Q8CHV5 | Q8CHV5 mus musculu |
| 9 | 190 | 10.6 | 328 | 5 Q8ITP3 | Q8ITP3 brachiocto |
| 10 | 189.5 | 10.5 | 277 | 6 Q8MTU1 | Q8MTU1 felis silve |
| 11 | 187.5 | 10.4 | 302 | 13 Q91B89 | Q91B89 oncorhynch |
| 12 | 186.5 | 10.4 | 280 | 13 Q8JIS9 | Q8JIS9 oryzias lat |
| 13 | 184.5 | 10.2 | 182 | 6 Q77623 | Q77623 ovis aries |
| 14 | 184 | 10.2 | 290 | 13 Q8JIS8 | Q8JIS8 oryzias lat |
| 15 | 182.5 | 10.1 | 304 | 13 Q93415 | Q93415 gallus gall |
| 16 | 177.5 | 9.9 | 277 | 6 Q8MJC3 | Q8MJC3 oryctolagus |

| | | | | | |
|----|-------|-----|-----|-----------|--------------------|
| 17 | 172.5 | 9.6 | 276 | 11 Q9D089 | Q9D089 mus musculu |
| 18 | 172.5 | 9.6 | 276 | 11 Q99M47 | Q99M47 mus musculu |
| 19 | 172.5 | 9.6 | 280 | 13 Q8UG42 | Q8UG42 fugu rubrip |
| 20 | 172 | 9.6 | 277 | 11 Q93397 | Q93397 ratius norv |
| 21 | 172 | 9.6 | 343 | 11 Q9MU16 | Q9MU16 ratius norv |
| 22 | 170.5 | 9.5 | 280 | 13 Q8GWM9 | Q8GWM9 fugu rubrip |
| 23 | 169 | 9.4 | 312 | 4 Q86UJ3 | Q86UJ3 homo sapien |
| 24 | 166.5 | 9.2 | 289 | 5 Q86FL0 | Q86FL0 anopheles s |
| 25 | 165 | 9.2 | 303 | 11 Q88550 | Q88550 ratius norv |
| 26 | 158.5 | 8.8 | 282 | 13 Q98U18 | Q98U18 brachydanio |
| 27 | 152.5 | 8.5 | 182 | 12 Q99CX0 | Q99CX0 bovine herp |
| 28 | 141 | 7.8 | 299 | 5 Q81955 | Q81955 spodoptera |
| 29 | 140 | 7.8 | 308 | 5 Q9NHP9 | Q9NHP9 drosophila |
| 30 | 140 | 7.8 | 308 | 5 Q9GV88 | Q9GV88 drosophila |
| 31 | 134.5 | 7.5 | 293 | 5 Q819V7 | Q819V7 bombyx mori |
| 32 | 130 | 7.2 | 189 | 11 Q8BN14 | Q8BN14 mus musculu |
| 33 | 114.5 | 6.4 | 316 | 5 Q817B0 | Q817B0 geodia cydo |
| 34 | 110 | 6.1 | 345 | 16 Q8E620 | Q8E620 streptococc |
| 35 | 110 | 6.1 | 345 | 16 Q8E0E6 | Q8E0E6 streptococc |
| 36 | 108 | 6.0 | 326 | 5 Q9GV88 | Q9GV88 hydra atten |
| 37 | 108 | 6.0 | 345 | 2 Q54085 | Q54085 streptococc |
| 38 | 107 | 5.9 | 188 | 12 P88961 | P88961 kapoti's sa |
| 39 | 103 | 5.7 | 283 | 13 Q42284 | Q42284 gallus gall |
| 40 | 103 | 5.7 | 347 | 5 Q9GV89 | Q9GV89 hydra atten |
| 41 | 100.5 | 5.6 | 344 | 2 Q57369 | Q57369 borrelia bu |
| 42 | 98 | 5.4 | 206 | 4 Q86WP4 | Q86WP4 homo sapien |
| 43 | 95.5 | 5.3 | 335 | 16 Q7VAV9 | Q7VAV9 prochloroco |
| 44 | 94.5 | 5.2 | 104 | 4 Q9UC96 | Q9UC96 homo sapien |
| 45 | 92 | 5.1 | 281 | 16 Q8XK49 | Q8XK49 clostridium |

ALIGNMENTS

RESULT 1

Q99MZ5 PRELIMINARY; PRT; 218 AA.
ID Q99MZ5
AC Q99MZ5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE FLIP short form.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Xiao C.W., Asselin E., Teang B.K.;
RT "FLIP mRNA expression in rat ovarian granulosa cells."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244366; AK28358.1;
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR001875; DED.
DR Pfam; PFO1335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; PSS0168; DED; 2.
SQ SEQUENCE 218 AA; 24718 MW; 9DA9EBAF3441967B CRC64;

Query Match 19.2%; Score 345; DB 11; Length 218;
Best Local Similarity 67.3%; Pred. No. 9.2e-20;
Matches 76; Conservative 15; Mismatches 18; Indels 4; Gaps 3;
QY 1 MARIGEDLPKSDVSLIFLMKDYMGKISKESFLDLVLEKLNLTAVAPDLDLEKCL 60
DB 102 LMEIGENLNQSDVSLIFLTXYTRGKAKXKSLDLVLEKLNLTGSGQNLNEKCL 161
QY 61 KNHRIIDLTKIQKQVQAGTSTRYNLQAIOK-SLKQPSNNFRE-EPV 110
DB 162 KSHRIDLTKIQKQVQAGTSTRYNLQAIOK-SLKQPSNNFRE-EPV 110

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RESULT 2
ID 08MJ18 PRELIMINARY; PRT; 78 AA.
AC 08MJ18;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Flce/caspase-1 inhibitory protein (Fragment).
OS Macaca mulatta (rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnould D., Lelievre J.-D., Lecocqier D., Hance A.J.,
RA Moneaux V., Ho Tsong Fang R., Hurtrel B., Amelien J.-C.,
RA Estquier J.;
RT "Caspase-dependent and -independent cell death pathways characterize
RT pathogenic Simian Immunodeficiency Virus infection. Relationship with
RT disease evolution."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF530077; AAA95637.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 78 AA; 8971 MW; 6BD208095733A99 CRC64;

Query Match 15.4%; Score 277; DB 6; Length 78;
Best Local Similarity 73.1%; Pred. No. 7.3e-15;
Matches 57; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 86 YNNVLQAAIQKSLKDPNNFR-----EPPYKSIQSEAFLPQSIPE 127
DB 1 YNNVLQAAIQKSLKDPNNFRLLHNGRSKQKQLQGPVKTSLQSEAFLPQSIPE 60
QY 128 ERYKMKSKPLGICLITDC 145
DB 61 ERYKMKSKPLGICLITDC 78

RESULT 3
ID 093417 PRELIMINARY; PRT; 283 AA.
AC 093417;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Caspase-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20149872; PubMed=10684799;
RA Johnson A.L., Bridgman J.T.;
RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa
RT cells."
RL Biol. Reprod. 62:589-598 (2000).
DR EMBL, AF083029; AAC32602.1; -.
DR HSSP, P42574; 1PAU.
DR MEROPS, C14.003; -.
DR GO, GO:0030693; F:caspase activity; IEA.
DR GO, GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro, IPR002138; ICF_P10.
DR InterPro, IPR001309; ICF_P20.
DR InterPro, IPR002398; Peptidase_C14.
DR Pfam, PF00656; Peptidase_C14; 1.
DR PRINTS, PR00376; IL1BCENZME.
DR SMART, SM00115; CASc; 1.
DR PROSITE, PS01122; CASPASE_CYS; 1.

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DR PROSITE, PS01121; CASPASE_HIS; 1.
DR PROSITE, PS50207; CASPASE_P10; 1.
DR PROSITE, PS50208; CASPASE_P20; 1.
SQ SEQUENCE 283 AA; 31675 MW; 161242DDEFD4DC4F CRC64;

Query Match 11.9%; Score 214; DB 13; Length 283;
Best Local Similarity 29.5%; Pred. No. 4.1e-09;
Matches 70; Conservative 31; Mismatches 92; Indels 44; Gaps 8;

QY 101 PSNNPREPPYKSIQSEAFLPQSIPEERYKMKSKPLGICLITDCIGNETELRPT----- 156
DB 22 PGSKGMPLPSKSVDSG-----ILPDDYRNDYRIGVCYI-----NNKMFHPTGLSS 71
QY 157 -----FTSLGYEQKPLHLSMAGISQILQFACMPHRYDSPFCVLYSRG 202
DB 72 RSGTDDAASVREVFMKLGKYKVLNNDLSRDIPLKLVRS-EEDHSKRSFVCVLLSHG 130
QY 203 GSGSYGVQVQTHSGULHHRIRMFQDSCPYLAGKPKFFQNYVYSGQLDSLSLEVD 262
DB 131 DEGLFQTD--GPLELKVLTSLFQDKCRSLAGKPLFTIO--ACGTGLDSLEADS 184
QY 263 GPAMKWEFAQKRGKCTVHREDFPWSLCTADMSILQSHSPSLYQCLSQKLRQ 319
DB 185 GPD-----ETVCCK-----IPVADFLYAVSTAPGYYSRMNAEGSWFTQSLCRMUK 232

RESULT 4
ID 091B66 PRELIMINARY; PRT; 303 AA.
AC 091B66;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Caspase-6.
GN XCASPAS-6.
OS Xenopus laevis (African Clawed Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family."
RL J. Biol. Chem. 275:10484-10491 (2000).
DR EMBL, AB038169; BA94747.1; -.
DR HSSP, P42574; ICP3.
DR MEROPS, C14.005; -.
DR GO, GO:0030693; F:caspase activity; IEA.
DR GO, GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro, IPR002138; ICF_P10.
DR InterPro, IPR001309; ICF_P20.
DR InterPro, IPR002398; Peptidase_C14.
DR Pfam, PF00656; Peptidase_C14; 1.
DR PRINTS, PR00376; IL1BCENZME.
DR SMART, SM00115; CASc; 1.
DR PROSITE, PS01122; CASPASE_CYS; 1.
DR PROSITE, PS01121; CASPASE_HIS; 1.
DR PROSITE, PS50207; CASPASE_P10; 1.
DR PROSITE, PS50208; CASPASE_P20; 1.
SQ SEQUENCE 303 AA; 34132 MW; 4C54A0A607C69756 CRC64;

Query Match 11.1%; Score 199; DB 13; Length 303;
Best Local Similarity 27.1%; Pred. No. 7.1e-08;
Matches 64; Conservative 41; Mismatches 101; Indels 30; Gaps 9;

QY 99 KDPNNPREPPYKSIQSEAFLPQSIPEERYKMKSKPLGICLITDC----- 144
DB 16 KDSIASENKEQKANTVETDGTWTSRTVELDPAEAYIMTKRGALIFTHEDFYVQLRLG 75
QY 145 -CIGNETEL--LNDFTSLGYEQKPLHL-SWNGISQILGQACMPHRYDSPFCVLYVS 200

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Dh 76 SRRGNTDSSNNLILTLDPDQVQNNYNTKTMVLEKI--QEAISTDHSNACCFICVPLIS 133
Qy 201 RGSQSYVYVDQTHSGPLPHHIRMFMWGDSCPYLAGPKMFFQNYVSDGQLEDSSL- 259
Dh 134 HGEKHIYSYV---SLIDIGELTNPFKGDCKSLVCKPFIILQ---AARGKHDEPVLP 187
Qy 260 --EVDGAMKNVKAQKRGCLCTVHRADPFWSLCTADMSLLEQSHSSPSLYLQCL 313
Dh 188 KDEVDSPVLTNTVLT-EVDASLCTLPAGADPFIMCYSVAGYSHRETVNSWYIIDL 242

RESULT 5

Q95NDS PRELIMINARY; PRT; 277 AA.
AC Q95NDS
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21334413; PubMed=11440638;
RA Muneta Y., Shimojima Y., Mori Y.;
RT "Porcine caspase-3: cloning and its activity during apoptosis of
RT porcine Pk15 cells induced by porcine Fas-119ad."
RL J. Interferon Cytokine Res. 21:409-415(2001).
DR EMBL; AB029345; BAB55544.1; -
DR MEROPS; C14.003; -
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Interpro; IPR002138; ICE_P10.
DR Interpro; IPR001309; ICE_P20.
DR Interpro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PRO0376; IL1BCENZME.
DR SMART; SMO0115; CASC.1.
DR PROSITE; PS0112; CASPASE_CYS; 1.
DR PROSITE; PS0112; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;

Query Match 10.8%; Score 193.5; DB 6; Length 277;
Best Local Similarity 29.4%; Pred. No. 1.8e-07;
Matches 63; Conservative 30; Mismatches 72; Indels 49; Gaps 9;

Qy 130 YKMSKPLDGLIILID-----C-IGNETEL--LRDTFTSLGYEV-----QKF 167
Dh 37 YKMDYPMGCIILNNKMPDKTGMACRSQTDVDANLAFETFTNLKYEVRNKNQDLTREFI 96
Qy 168 LHLMSHGISQILGQFACMPERHRYDSFVCLVSRGSGSYVGVDTGHSGLPHHIRRFM 227
Dh 97 LEL-MHSVSK-----EDHSKRSSFICVLSHGEGKIFG---TNGVVDLKKLITSPFR 144
Qy 228 GDSCPYLAGPKMFFIQ--NYVSDQLEDSSLLEVDPAMKNVKAQKRGCLCTVHREA 285
Dh 145 GDCRRTLTGPKFIILQACRGCTELDGIETDSDTEEDMACQK-----IPVEA 191
Qy 286 DFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQ 319
Dh 192 DFLVAYSTAGYYSWRNSKDGSWFIQSLCALKQ 225

RESULT 6
Q91B65 PRELIMINARY; PRT; 318 AA.
AC Q91B65;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-7.
GN XCASPASE-7.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OC Xenopodidae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family."
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038170; BAB94748.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.004; -
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Interpro; IPR002138; ICE_P10.
DR Interpro; IPR001309; ICE_P20.
DR Interpro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PRO0376; IL1BCENZME.
DR SMART; SMO0115; CASC.1.
DR PROSITE; PS0112; CASPASE_CYS; 1.
DR PROSITE; PS0112; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 318 AA; 35937 MW; 6EB06684F86A128 CRC64;

Query Match 10.7%; Score 192.5; DB 13; Length 318;
Best Local Similarity 27.6%; Pred. No. 2.5e-07;
Matches 64; Conservative 39; Mismatches 92; Indels 37; Gaps 10;

Qy 111 KKSIOSEAFLPDSI-----PEERYKMSKPLDGLIILID-----CIG-----NETE 151
Dh 48 KKVEDEKPKPTNNNVAIVTAPQYKNNNGVGRCTIINKKIFDKITGNGARNGTIDARE 107
Qy 152 LNRDTFTSLGYEVQKPLHLSMGIISQILGQFACMPERHRYDSFVCLVSRGSGSYVD 211
Dh 108 LNR-CFKGLGFVDVNVNKNKSCSEMENLITVA-QQDHKDSACFACIFLSHGEGLIYGD 165
Qy 212 QTHSGPLPHHIRMFMWGDSCPYLAGPKMFFIQ--NYVSDQLEDSSLLEVDPAMK 267
Dh 166 ---GAMPIKIVLTILFEGDNCRLVGRKPLFIQACRGHFDG-----LEADSGSYVD 215
Qy 268 NVEFKQKRGCLCTVHREADPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQ 319
Dh 216 SLETDANPRHKIPV--EADFLVAYSTVPGYYSWRNPMGMSWFCALCSVLNE 265

RESULT 7

Q8WK15 PRELIMINARY; PRT; 277 AA.
AC Q8WK15;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Sano J.;
RT "canine caspase-3 gene."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB085580; BAB92962.1; -
DR GO; GO:0030693; F:caspase activity; IEA.

DR GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBENZYM.
 DR SMART; SMO0115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 277 AA; 31334 MW; 7094C76D868DBA9 CRC64;

Query Match 10.7%; Score 192; DB 6; Length 277;
 Best Local Similarity 26.9%; Pred. No. 2,3e-07;
 Matches 64; Conservative 38; Mismatches 92; Indels 44; Gaps 8;

QY 102 SNRPBPPVKK---KSIQSEAFLLPQSIPEBRYKMKKPLGICLIID----- 144
 DB 10 AKSFNAAETKILHSGSKVDSQMSF-----DMSYKMDYPEMGICIIINKNPFKSTGMAP 63
 QY 145 CIGNTEL--LRDFTSLGYEVQKFLHSMHGISQILGQFACMPEHRDYSFVCVLSRG 202
 DB 64 RSGTVDANLRETTINKLVKRNKNDLTCEELILNVSYS-KEDSKSKSFVCVLSHG 122
 QY 203 GSQVYGVDTGSHGLPLHHRMFMGDSCPYLAKKPMFTIQ--NYVSDQLEDSSLLIE 260
 DB 123 DEGIIFG--TNGPVDLRKVTGPRGDYCRSLTKPFLIQCRGTLEDGCIETDSGIE 179
 QY 261 VDGPMKVERFAQKRGICITVHRADPFWSLCTADMSLLEQSHSSPSLYLQCSQKLR 318
 DB 180 DWMACQK-----IPVADFLVAYSTAPGYYSWRNSKDSWFIQSLCMLK 224

RESULT 8

Q8CHVS PRELIMINARY; PRT; 313 AA.
 AC Q8CHVS;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Caspase 3, apoptosis related cysteine protease (Fragment).
 GN CASP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RA Strausberg R.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC038825; AAH38825.1; -.
 DR MGD; MGI:107739; Casp3.
 DR GO; GO:0030693; P:caspase activity; IEA.
 DR GO; GO:008223; P:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBENZYM.
 DR SMART; SMO0115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Protease.
 FT NON TER
 SQ SEQUENCE 313 AA; 35174 MW; 96B98A1F04E769FC CRC64;

Query Match 10.6%; Score 190.5; DB 11; Length 313;
 Best Local Similarity 28.5%; Pred. No. 3.6e-07;

Matches 75; Conservative 40; Mismatches 107; Indels 41; Gaps 13;
 QY 76 KQSVQAGT---SYRWLQAAIQSLKDPSS-NNFREEPV--KSIQSEAFLLPQSIPEB 129
 DB 19 KRSVLKRGAMNGTLRVTYNNKTSYVDSISINFEVKITHGSKY-DGIIYLDSS----- 72
 QY 130 YKXKSRPLGICLIID-----CIGNTEL--LRDFTSLGYEVQKFLHSMHG 175
 DB 73 YKMDYPEMGICIIINKNPFKSTGMSRSGTVDANLRETFMGILKYQVRKNDLTREDI 132
 QY 176 SQLGQFACMPEHRDYSFVCVLSRGSGSQSYGVDTGSHGLPLHHRMFMGDSCPYLA 235
 DB 133 LEIWDVSYS-KEDSKSKSFVCVLSHGDEGVYQ--TNGPVELKLTNSFRGDYCRSLT 188
 QY 236 GKPRMFTIQNYVSDQLEDSSLLIEVDGPMKVERFAQKRGICITVHRADPFWSLCTAD 295
 DB 189 GKPRLFTIQ--ACRGTLEDGCIETDSGT--DEMACQK-----IPVADFLVAYSTAP 237
 QY 296 MSLLSQSHSSPSLYLQCSQKLR 318
 DB 238 GYYSWRNSKDSWFIQSLCMLK 260

RESULT 9

Q8ITP3 PRELIMINARY; PRT; 328 AA.
 AC Q8ITP3;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE AmphicASP-3/7.
 OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 OX NCBI_Taxid=7739;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22217375; Pubmed=12232796;
 RA Bayascas J.R., Yuste V.J., Benito E., Garcia-Fernandez J.,
 RA Comella J.X.;
 RT "Isolation of AmphicASP-3/7, an ancestral caspase from amphioxus
 RT (Branchiostoma floridae). Evolutionary considerations for vertebrate
 RT caspases.";
 RT Cell Death Differ. 9:1078-1089(2002).
 DR EMBL; AF412335; AAN45849.1; -.
 DR GO; GO:0030693; P:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBENZYM.
 DR SMART; SMO0115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 328 AA; 36327 MW; 1D46760AF471845B CRC64;

Query Match 10.6%; Score 190; DB 5; Length 328;
 Best Local Similarity 32.7%; Pred. No. 4.1e-07;
 Matches 55; Conservative 24; Mismatches 77; Indels 12; Gaps 6;

QY 157 FTSLGVEVQKFLHSMHGISQILGQFACMPEHRDYSFVCVLSRGSGSYGVDTGSHG 216
 DB 120 FSKLGFEFTKVFDNLPCKILSVL-QLAARDHRDVCFCALISHGEEGVIGTD----GH 175
 QY 217 LPLHHRMFMGDSCPYLAKKPMFTIQNYVSDQLEDSSLLIEVDGPMKVERFAQK 275
 DB 176 MEVTEVTKPRGRCPELVGKPRFLFQ--ACRGNFPHG--VMDPALFEVQDELDA 229
 QY 276 RGLCTVHRADPFWSLCTADMSLLEQSHSSPSLYLQCSQKLRQERGT 323

Db 230 GNRKTLPAEADFLIATSTVPGYYSWRNPGRGSWYIQAALCAVIERE-GT 276

RESULT 10

Q8MTJ1 PRELIMINARY; PRT; 277 AA.

AC Q8MTJ1

DT 01-OCT-2002 (Tremblrel. 22, Created)

DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Caspase3.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

NCBI_TaxID=9685;

QX NCBI_TaxID=9685;

QY SEQUENCE FROM N.A.

RA Yamazaki J., Sano R., Hasegawa A.;

RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB090246; F:caspace activity; IEA.

DR GO: GO:0030693; F:caspace activity; IEA.

DR GO: GO:0006508; F:proteolysis and peptidolysis; IEA.

DR InterPro: IPR002138; ICE_p10.

DR InterPro: IPR001309; ICE_p20.

DR InterPro: IPR002398; Peptidase C14.

DR Pfam: PF00656; Peptidase C14; I.

DR PRINTS: PR00376; ILIBCNZYME.

DR SMART: SM00115; CASc; 1.

DR PROSITE: PS01121; CASPASE_CYS; 1.

DR PROSITE: PS01121; CASPASE_HIS; 1.

DR PROSITE: PS50207; CASPASE_P10; 1.

DR PROSITE: PS50208; CASPASE_P20; 1.

QY SEQUENCE 277 AA; 31465 MW; 8749679C30AB46F6 CRC64;

QZ

Query Match 10.5%; Score 189.5; DB 6; Length 277;

Best Local Similarity 27.8%; Pred. No. 3,7e-07;

Matches 66; Conservative 35; Mismatches 83; Indels 53; Gaps 9;

QY 112 KSIOSEAPF---PQSIIP-----EERYKMKSKRIGLCILID-----CIGNETE 151

Db 11 KSINKSSTKTFHSGSKSDSGIYNDNSYKMDYPMWGLCIINKNHSTGMPRSSTVDV 70

QY 152 L--LRDFTSLGYEVOKFHLTHSMHGISQILGQFACPEHRDYSFVCYLVRGSGSQSYG 209

Db 71 AANLRFTFLTKYEVANKNDLTREQIVALLDSYS-REDHSKSSSFICVLLSHGEEGIY 129

QY 210 VDOTHSGLPLHTRKRMENGDSCPYLAGKRMFIQNY-----VSDGQLEDSLLLEV 261

Db 130 ---TNGVVDIKKLTGFRRGYCRSLGKPKFLIQCRCGTLDGCIETDSGTED----- 180

QY 262 DGPAMKVEFKAKRGICLTVHREADPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLR 318

Db 181 -----DIACK-----IPVADFLVYSTAPGYYSWRNKGDSWFIQSLCSMLR 224

RESULT 11

Q918S9 PRELIMINARY; PRT; 302 AA.

AC Q918S9

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Caspase 6.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

NCBI_TaxID=8022;

QX NCBI_TaxID=8022;

QY SEQUENCE FROM N.A.

RA Iain K.J., Holland J., Bonilla S., Cunningham C., Secombes C.D.;

RL Cloning and sequencing of caspase 6 in rainbow trout, *Oncorhynchus*

RT mykiss, and analysis of its expression under conditions known to induce apoptosis.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF212219; AAF73848.1; -

DR HSPD: P42574; 1PAU.

DR MER08; C14.005; -.

DR GO: GO:0030693; F:caspace activity; IEA.

DR GO: GO:0006508; F:proteolysis and peptidolysis; IEA.

DR InterPro: IPR002138; ICE_p10.

DR InterPro: IPR001309; ICE_p20.

DR InterPro: IPR002398; Peptidase C14.

DR Pfam: PF00656; Peptidase C14; I.

DR PRINTS: PR00376; ILIBCNZYME.

DR SMART: SM00115; CASc; 1.

DR PROSITE: PS01121; CASPASE_CYS; 1.

DR PROSITE: PS01121; CASPASE_HIS; 1.

DR PROSITE: PS50207; CASPASE_P10; 1.

DR PROSITE: PS50208; CASPASE_P20; 1.

QY SEQUENCE 302 AA; 34082 MW; 5A6B5F28ACFA660 CRC64;

QZ

Query Match 10.4%; Score 187.5; DB 13; Length 302;

Best Local Similarity 25.0%; Pred. No. 5,9e-07;

Matches 69; Conservative 38; Mismatches 110; Indels 59; Gaps 10;

QY 67 DLKTKIQKYSQVQAGTSYRVVLQAIQKSLKDESNPFREPYVKSIQSEAPFLPSI- 125

Db 8 DTGSLKQNKTSQTTG-----PSEN-----ITEDGFCSSSF 41

QY 126 ---FEERYMKSKRPLGICILID-----CIGNETELRDFTSLGYEVOKF 167

Db 42 SMDPAEYKMKRRLALIFQEHFVHLMPRNGNADRSNLVK-RFEDLNEVQAF 100

QY 168 LHLTHSMGICQILGQF--ACMPEHRDYSFVCYLVRGSGSQSYGVDTQHSGLPLHTRM 225

Db 101 DNLR---VEEVLDDQSQAENAHADCFVCFVLSHGNDHYAYDK--IAIDITAL 154

QY 226 FMDSCSPYLAGKPKRPFIONVYVSDGLEDSL--LEVDCPAMKVEFKAKRGICTVHR 283

Db 155 FKGDCKSLVGKPKFILO--ACRGDKHDPVTMDVDESVKNEVYVAGVYITLPA 211

QY 284 EADPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQ 319

Db 212 GADFMCVSAEGYVSHRETLINGSWYIQLDLCAMRK 247

RESULT 12

Q8JIS9 PRELIMINARY; PRT; 280 AA.

AC Q8JIS9

DT 01-OCT-2002 (Tremblrel. 22, Created)

DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Caspase 3B.

OS Oryzias latipes (Medaka fish) (Japanese ricefish).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

NCBI_TaxID=8090;

QX NCBI_TaxID=8090;

QY SEQUENCE FROM N.A.

RA MEDLINE=20211495; PubMed=10747068;

RA Naruse K., Fukumachi S., Mitani H., Kondo M., Matsuo K., Kondo S., Hanamura N., Morita Y., Hasegawa K., Nishigaki R., Shimada A., Wada H., Kusabe T., Suzuki N., Kinoshita M., Kanamori A., Terado T., Kimura H., Nonaka M., Shima A.;

RL Detailed linkage map of Medaka, *Oryzias latipes*: Comparative genomics and genome evolution.";

RT Genomics 154:1773-1784(2000).

DR EMBL: AB032608; BAC00948.1; -

DR GO: GO:0030693; F:caspace activity; IEA.

DR GO: GO:0006508; F:proteolysis and peptidolysis; IEA.

DR InterPro: IPR002138; ICE_p10.

DR InterPro; IPR001309; ICE p20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR PRINTS; PR00376; TLIBCNZYME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 280 AA; 31168 MW; 5095512F1E485542 CRC64;

Query Match 10.4%; Score 186.5; DB 13; Length 280;
 Best Local Similarity 27.5%; Pred. No. 6.5e-07;
 Matches 61; Conservative 26; Mismatches 74; Indels 61; Gaps 9;

QY 129 RYKMSKRLGICLIIDICNETELLRD-----FTSLGYEVOKFLHL 170
 DB 43 RYSLNFPITGLCIIL-----NNKNPDRGTGMNNGNDIDASAAMKVFSLGFRVKTLYNQ 98
 QY 171 SMHGISQILGQFACMPERHDYDSFVCLVSRGSGSYGVDTQHSGLPLHIRRMFGDS 230
 DB 99 TVKQIKQLITDVSRN-DHSDASFCVILSHGEGVFFGTD--GSIELKTLTSLFRGDH 154
 QY 231 CEYLAKRPMFIONVYVSDGLSDSLLEVDPGAMKNVEFKAQKRGKGLCTVHREADPFWS 290
 DB 155 CKSLVGKPKLFFIQ--ACRGTELDG--LEAD-----SKEDTTKIPVENDFLYA 199
 QY 231 LCTADMSLLEQSHSSPSLYLQCLSGKLRGRTIPSGSITES 332
 DB 200 FSTA-----PGY-----SWRNTWTGSMFIN 221

RESULT 13

077623 PRELIMINARY; PRT; 182 AA.

AC 077623;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Caspase-3 (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rueda B.R., Hendry I.R., Tilly J.L., Hamernik D.L.,
 RT "Accumulation of Caspase-3 mRNA and induction of Caspase Activity in
 the Ovine Corpus Luteum Following Prostaglandin-F2a Treatment in
 Vivo."
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF068637; AAC25713.1; -
 DR HSSP; P42574; 1PAU.
 DR MEROPS; C14.003; -
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002398; ICE p10.
 DR InterPro; IPR001309; ICE p20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 FT NON TER 1 1
 SQ SEQUENCE 182 AA; 20408 MW; B5860C6996C21BE7 CRC64;

Query Match 10.2%; Score 184.5; DB 6; Length 182;
 Best Local Similarity 31.0%; Pred. No. 5.5e-07;
 Matches 57; Conservative 27; Mismatches 67; Indels 33; Gaps 7;

QY 127 EERYKXKSLPLGICLIID-----C-IGNTEL--LRDTFTSLGYEVOKFLHSM 172
 DB 3 EESYKQIDYEMGICLIHNNKNFNHNTGMACRSGIDVDANIRFETFTSLKYVRIRKNDLTR 62
 QY 173 HGISQILGQFACMPERHDYDSFVCLVSRGSGSYGVDTQHSGLPLHIRRMFGDSCP 232
 DB 63 KEMLEMSDV5-KEDSKRSSTFCVILSHGEGVFFGTD--INGPYDLXKLASFRRGDCC 118
 QY 233 YLAKRPMFIIQ--NYVSDGQLSDSLLEVDPGAMKNVEFKAQKRGKGLCTVHREADPFWS 290
 DB 119 SLTGKPKLFLIQACRGTELDGIFETDSGEDDMACQ-----IPVADFLYA 165
 QY 291 LCTA 294
 DB 166 YSTA 169

RESULT 14

080158 PRELIMINARY; PRT; 290 AA.

AC 080158;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Caspase 3A.
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20211495; PubMed=10747068;
 RA Natuse K., Fukumachi S., Mitani H., Kondo M., Matsuo T., Kondo S.,
 RA Hanamura N., Morita Y., Hasegawa K., Nishigaki R., Shimada A.,
 RA Wada H., Kusakabe T., Suzuki N., Kinoshita M., Kanamori A., Terada T.,
 RA Kimura H., Nonaka M., Shima A.;
 RT "A detailed linkage map of Medaka, Oryzias latipes: Comparative
 Genomics and Genome Evolution."
 RL Genetics 154.1:173-1784 (2000).
 DR EMBL; AB032609; BAC0949.1; -
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002398; ICE p10.
 DR InterPro; IPR001309; ICE p20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR PRINTS; PR00376; TLIBCNZYME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 290 AA; 32686 MW; D6CB3C00D2E846C CRC64;

Query Match 10.2%; Score 184; DB 13; Length 290;
 Best Local Similarity 25.4%; Pred. No. 1.1e-06;
 Matches 62; Conservative 41; Mismatches 99; Indels 42; Gaps 7;

QY 97 SLNDPSN--NFRREPYSKSIQSEAFPLPSIPERYKMSKRLGICLI----- 143
 DB 23 SKSPANQPPRSTDCYVKKQDDPR-----RSMQYPRKGCILIIINNKNPFKDSGM 74
 QY 144 ---DCIGNETELLRDFTFTSLGYEVOKFLHSMHGISQILGQFACMPERHDYDSFVCLV 200
 DB 75 GFRNGTDNDAAAMKSPMKLGYEIQMNYQTVDQMKELFRQMS-NQDSKRFASFCVILS 133
 QY 201 RGSQSYGVDTQHSGLPLHIRRMFGDSCPYLKGKPMFFIONVYVSDGLSDSLLE 260
 DB 134 HGEQGVYFQD---GPVSFKLLECKLKGSSCLSLVGKPKLFFIQ--ACRGMLFD----- 182
 QY 261 VDPGAMKNVEFKAQKRGKGLCTVHREADPFWSLCTADMSLLEQSHSSPSLYLQCLSGKLR 320

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2004, 05:51:33; Search time 128 Seconds
(without alignments)
768.176 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDLDKSVSLIFLM.....ITSEKDMFESSLGICLLDVL 348

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1312285

Minimum DB seq length: 0
Maximum DB seq length: 348

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Genesegp290a04:*
2: Genesegp1980s:*
3: Genesegp1990s:*
4: Genesegp2000s:*
5: Genesegp2001s:*
6: Genesegp2002s:*
7: Genesegp2003s:*
8: Genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 1800 | 100.0 | 348 | 2 | AAW69230 I-FLICE-2 |
| 2 | 1800 | 100.0 | 348 | 7 | ADA10619 Human inh |
| 3 | 1229 | 68.3 | 302 | 2 | AAV05792 WRIT-ND1 |
| 4 | 1128 | 62.7 | 264 | 2 | AAV05790 Human ant |
| 5 | 978 | 54.3 | 230 | 2 | AAV05793 MRIT-Bam |
| 6 | 711.5 | 39.5 | 291 | 3 | AAV67420 Usurpin-G |
| 7 | 683 | 37.9 | 175 | 2 | AAV05794 MRIT-D/S |
| 8 | 661.3 | 36.8 | 270 | 5 | AAE26110 Human FLA |
| 9 | 540 | 30.0 | 227 | 2 | AAV05795 WRIT Beta |
| 10 | 527 | 29.3 | 221 | 2 | AAW78904 Human GI |
| 11 | 527 | 29.3 | 221 | 2 | AAW76630 Human CFL |
| 12 | 527 | 29.3 | 221 | 2 | AAV05789 Human MAC |
| 13 | 527 | 29.3 | 221 | 2 | AAV57455 Human FLI |
| 14 | 527 | 29.3 | 221 | 3 | AAV03959 FLICE-lik |
| 15 | 527 | 29.3 | 221 | 4 | AAE61117 Human MRI |
| 16 | 527 | 29.3 | 221 | 4 | AAE61117 Human MRI |
| 17 | 527 | 29.3 | 221 | 5 | ABBO9293 Human FLI |
| 18 | 391 | 21.7 | 76 | 4 | AAAI5359 Peptide # |
| 19 | 391 | 21.7 | 76 | 4 | ABR34356 Peptide # |
| 20 | 391 | 21.7 | 76 | 4 | AAW78377 Peptide # |
| 21 | 391 | 21.7 | 76 | 4 | ABR39199 Peptide # |
| 22 | 391 | 21.7 | 76 | 4 | ABR19775 Protein # |
| 23 | 391 | 21.7 | 76 | 4 | AAE67546 Human Don |
| 24 | 391 | 21.7 | 76 | 4 | AAW51553 Human bra |
| 25 | 391 | 21.7 | 76 | 4 | ABG49189 Human liv |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 25 | 391 | 21.7 | 76 | 4 | AAW03118 |
| 27 | 391 | 21.7 | 76 | 5 | ABG37140 Human pep |
| 28 | 383 | 21.3 | 84 | 4 | ABR84787 MRIT deat |
| 29 | 369 | 20.5 | 84 | 4 | AAE61102 Human MRI |
| 30 | 337 | 18.7 | 218 | 5 | ABR09296 Mouse FLI |
| 31 | 228 | 12.7 | 286 | 3 | AAV56997 Human pro |
| 32 | 228 | 12.7 | 286 | 4 | AAV59578 Human cas |
| 33 | 225 | 12.5 | 254 | 4 | AAV86656 Caspase-8 |
| 34 | 215 | 11.9 | 266 | 2 | AAW11896 MACH isof |
| 35 | 199 | 11.1 | 293 | 2 | AAW06244 Apoptotic |
| 36 | 199 | 11.1 | 293 | 2 | AAV21720 Amino aci |
| 37 | 199 | 11.1 | 293 | 4 | AAE00603 Human cas |
| 38 | 199 | 11.1 | 293 | 5 | AAO21925 Human cas |
| 39 | 199 | 11.1 | 293 | 5 | ABJ01221 Human cas |
| 40 | 193.5 | 10.8 | 237 | 4 | AAV78712 Pig caspa |
| 41 | 190 | 10.6 | 231 | 5 | ABP42451 Human ova |
| 42 | 189.5 | 10.5 | 167 | 4 | AAW31155 Peptide # |
| 43 | 189 | 10.5 | 261 | 4 | AAE06810 Chimeric |
| 44 | 188.5 | 10.5 | 277 | 4 | AAU05395 Mouse cas |
| 45 | 187.5 | 10.4 | 278 | 3 | AAV85061 Interleuk |

ALIGNMENTS

RESULT 1
ID AAW69230 standard; protein; 348 AA.
AAW69230:
18-FEB-1999 (first entry)
I-FLICE-2 protein.
I-FLICE-2 protein.
I-FLICE-2: PADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease;
CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis;
CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease;
multiple sclerosis; head injury; cancer; autoimmune disorder; therapy;
viral infection; graft versus host disease; graft rejection.
Homo sapiens.
WO9831801-A1.
23-JUL-1998.
21-JAN-1998; 98WO-US000969.
21-JAN-1997; 97US-0034205P.
05-AUG-1997; 97US-0054800P.
(HUMA-) HUMAN GENOME SCI INC.
(UNMI) UNIV MICHIGAN.
N1 J, Rosen CA, Dixit VM, Gentz RL, Kenny JI;
WPI, 1998-414100/35.
N-PSDB; AAV4807.
New inhibitory polypeptides of FLICE - used to develop products for
treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis, cancers,
autoimmune disorders, viral infection or graft rejection.
Claim 9, Fig 4, 118pp. English.
This sequence is an inhibitor of Fas-ligand associated with death
domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-2. The
proteins can inhibit both TNFR-1 and CD-95 induced apoptosis. These are
the first examples of a naturally occurring catalytically inactive
caspase that can act as a dominant negative inhibitor of apoptosis. The
polypeptides and agonists can be used for treating e.g. Alzheimer's
disease, Parkinson's disease, rheumatoid arthritis, septic shock, sepsis,

CC stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
 CC cell death associated with cardiovascular disease, polycystic kidney
 CC disease, apoptosis of endothelial cells in cardiovascular disease,
 CC degenerative liver disease, multiple sclerosis (MS) and head injury
 CC damage. Antagonists of the polypeptides can be used for treating cancers
 CC (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-
 CC dependent tumours, and cancers of the breast, ovary, prostate, bone,
 CC liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic
 CC lupus erythematosus, immune-related glomerulonephritis, rheumatoid
 CC arthritis), and viral infections (e.g. herpes viruses, pox viruses and
 CC adenoviruses), graft versus host disease, acute disease, acute graft
 CC rejection, and chronic graft rejection. The products can also be used for
 CC detection, diagnosis and drug screening

CC Sequence 348 AA;

Query Match 100.0%; Score 1800; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 5.6e-172;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSLIFLMKDVMGRKISKSEKSFLDLVLEKLNVAPOQDLLEKCL 60
 DB 1 MAEIGEDLDKSDVSLIFLMKDVMGRKISKSEKSFLDLVLEKLNVAPOQDLLEKCL 60
 QY 61 KNHRIIDLTKIQKQKOSVQAGTSYRNVLQAAIQSLKDPNNFREBPVKKSIOSEBAF 120
 DB 61 KNHRIIDLTKIQKQKOSVQAGTSYRNVLQAAIQSLKDPNNFREBPVKKSIOSEBAF 120
 QY 121 LPOSIPERRYKMKSRPLGICLIIDICIGNETELRLDTFTSLGYEVQKFLHSMHGISOILG 180
 DB 121 LPOSIPERRYKMKSRPLGICLIIDICIGNETELRLDTFTSLGYEVQKFLHSMHGISOILG 180
 QY 181 QPACMEHRDYSFVCVLVSRGSGSVYGVDTHTSGPLPHIRRMFGDSCPYLAGPKM 240
 DB 181 QPACMEHRDYSFVCVLVSRGSGSVYGVDTHTSGPLPHIRRMFGDSCPYLAGPKM 240
 QY 241 FFIQNVVSDGQLDSSLSLEVDPAMKNVEFKAQKGLCTVHREAPFMSLCTADMSLLE 300
 DB 241 FFIQNVVSDGQLDSSLSLEVDPAMKNVEFKAQKGLCTVHREAPFMSLCTADMSLLE 300
 QY 301 QSHSSPSLYLQCLSQKLRQERGTIPSGGITESKDMHFSSIGCILLDVL 348
 DB 301 QSHSSPSLYLQCLSQKLRQERGTIPSGGITESKDMHFSSIGCILLDVL 348

RESULT 2

ADA10619 standard; protein; 348 AA.

AC ADA10619;

DT 06-NOV-2003 (first entry)

XX Human inhibitor of FLICE (I-FLICE-2) protein.

DE Human; I-FLICE-2; inhibitor of FLICE; FADD-like ICE;
 KM tumour necrosis factor receptor-1 inhibitor; TNFR-1 inhibitor;
 KM CD-95 induced apoptosis; apoptosis associated disease;
 KM Alzheimer's disease; rheumatoid arthritis; stroke; osteoporosis;
 KM ischaemia; septic shock; degenerative liver disease;
 KM cardiovascular disorder; aberrant cell survival; noctropic;
 KM antineutrotic; vasotropic; hepatotropic; osteopathic; cardiac;
 KM cerebroprotective; antibacterial; antiarthritic; vasodilator.

OS Homo sapiens.

XX US2003087339-A1.

XX 08-MAY-2003.

XX 21-JAN-1998; 98US-00009893.

XX 21-JAN-1997; 97US-0034205P.

PR 05-AUG-1997; 97US-0054800P.

PA (NUTJ/) NI J.
 PA (ROSE/) ROSEN C. A.
 PA (DIXI/) DIXIT V. M.
 PA (GENTZ/) GENTZ R. L.
 PA (KENNY/) KENNY J. J.

PI NI J, ROSEN CA, DIXIT VM, GENTZ RL, KENNY JU;

XX WPI; 2003-576674/54.

DR N-PSDB; ADA10618.

PT New I-FLICE-1 (inhibitor of FLICE 1) or I-FLICE-2 nucleic acids, useful
 PT for treating diseases associated with apoptosis e.g., Alzheimer's
 PT disease, rheumatoid arthritis, stroke, osteoporosis, ischemia or septic
 PT shock.

XX Claim 1; Fig 4A-4C; 48pp; English.

XX The present invention relates to the isolation of novel human I-FLICE-1
 CC (inhibitor of FLICE (FADD-like ICE)) and I-FLICE-2 proteins, and the
 CC polynucleotide sequences encoding them. The I-FLICE-1 and I-FLICE-2
 CC proteins are novel inhibitors of tumour necrosis factor receptor-1 (TNFR-
 CC 1) and CD-95 induced apoptosis. Also disclosed are vectors, host cells
 CC and recombinant methods for producing the I-FLICE proteins. The sequences
 CC and methods are useful for treating diseases associated with apoptosis
 CC e.g., Alzheimer's disease, rheumatoid arthritis, stroke, osteoporosis,
 CC ischaemia, septic shock, degenerative liver disease, and cardiovascular
 CC disorders. They are also useful for diagnosing diseases or disorders
 CC associated with aberrant cell survival in an individual. The present
 CC sequence represents human I-FLICE-2.

XX Sequence 348 AA;

Query Match 100.0%; Score 1800; DB 7; Length 348;
 Best Local Similarity 100.0%; Pred. No. 5.6e-172;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSLIFLMKDVMGRKISKSEKSFLDLVLEKLNVAPOQDLLEKCL 60
 DB 1 MAEIGEDLDKSDVSLIFLMKDVMGRKISKSEKSFLDLVLEKLNVAPOQDLLEKCL 60
 QY 61 KNHRIIDLTKIQKQKOSVQAGTSYRNVLQAAIQSLKDPNNFREBPVKKSIOSEBAF 120
 DB 61 KNHRIIDLTKIQKQKOSVQAGTSYRNVLQAAIQSLKDPNNFREBPVKKSIOSEBAF 120
 QY 121 LPOSIPERRYKMKSRPLGICLIIDICIGNETELRLDTFTSLGYEVQKFLHSMHGISOILG 180
 DB 121 LPOSIPERRYKMKSRPLGICLIIDICIGNETELRLDTFTSLGYEVQKFLHSMHGISOILG 180
 QY 181 QPACMEHRDYSFVCVLVSRGSGSVYGVDTHTSGPLPHIRRMFGDSCPYLAGPKM 240
 DB 181 QPACMEHRDYSFVCVLVSRGSGSVYGVDTHTSGPLPHIRRMFGDSCPYLAGPKM 240
 QY 241 FFIQNVVSDGQLDSSLSLEVDPAMKNVEFKAQKGLCTVHREAPFMSLCTADMSLLE 300
 DB 241 FFIQNVVSDGQLDSSLSLEVDPAMKNVEFKAQKGLCTVHREAPFMSLCTADMSLLE 300
 QY 301 QSHSSPSLYLQCLSQKLRQERGTIPSGGITESKDMHFSSIGCILLDVL 348
 DB 301 QSHSSPSLYLQCLSQKLRQERGTIPSGGITESKDMHFSSIGCILLDVL 348

RESULT 3

AAV05792 standard; protein; 302 AA.

XX AAV05792;

XX 02-AUG-1999 (first entry)

DE MMT-ND1 polypeptide.

XX MRIT-ND1, MACH related inducer of toxicity; human; apoptosis;
 KM anti-apoptotic; cancer; autoimmune disease; angiogenesis;
 KM atherosclerosis; neurodegenerative disease; Alzheimer's disease;
 KM Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
 KM aplastic anaemia; myocardial infarction; therapy; mutant.

XX Homo sapiens.
 OS Synthetic.

PN W09918230-A2.

PD 15-APR-1999.

PF 07-OCT-1998; 98MO-US021132.

PR 07-OCT-1997; 97US-00946226.

PA (UNIW) UNIV WASHINGTON.

PI Chaudhary PM;

DR WPI; 1999-277275/23.

PT Identifying regulators of MACH-related inducer of toxicity.

PS Example 2; Page; 78pp; English.

XX The present sequence represents MRIT-ND1, comprising amino acid residues
 CC 179-480 of novel human MACH-related inducer of toxicity MRIT alpha 1 (see
 CC AAY05787). This deletion mutant was used to examine the interaction of
 CC MRIT alpha 1 with caspases. The results indicated that FRIC-p20 binding
 CC to MRIT alpha 1 does not require the N-terminal 179 amino acids. The
 CC invention provides multiple isoforms of MRIT (see AAY05787-89), isolated
 CC active fragments of which have either pro-apoptotic or anti-apoptotic
 CC activity. Selective enhancers and inhibitors of MRIT apoptotic activity
 CC can be identified and used to treat diseases mediated by the dysfunction
 CC of programmed cell death or proliferation, such as cancer or a
 CC neurodegenerative disorder. Note: the present sequence is not shown in
 CC the specification but is derived from the MRIT alpha 1 sequence given in
 CC figure 1F

XX Sequence 302 AA;

Query Match 68.3%; Score 1229; DB 2; Length 302;
 Best Local Similarity 92.2%; Pred. No. 1.2e-114;
 Matches 237; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 83 GTSYRNVLQALIQKSLKDPNNR-----EEVYKSIQSEAFIPQS 124

DB 1 GTSYRNVLQALIQKSLKDPNNRFLHNGSKRQLEQIGAQCEPVKKSIOSEAFIPQS 60

QY 125 IPEERYKMSKPLGICLIIDICIGNETELDRDFTSLGYEVQKFLHSMHGISOILGQFAC 184

DB 61 IPEERYKMSKPLGICLIIDICIGNETELDRDFTSLGYEVQKFLHSMHGISOILGQFAC 120

QY 185 MPEHRDYDSVVCVLVSRGSSQSVYGVDTQHSGLPLHHRMFMGDSQCYLLAGKPMFEITQ 244

DB 121 MPEHRDYDSVVCVLVSRGSSQSVYGVDTQHSGLPLHHRMFMGDSQCYLLAGKPMFEITQ 180

QY 245 NYVVSQGLDESSLLEVDPGPAKNVFEKAKRGKGLCTVHREADFEWLSCTADMSLLEQSHS 304

DB 181 NYVVSQGLDESSLLEVDPGPAKNVFEKAKRGKGLCTVHREADFEWLSCTADMSLLEQSHS 240

QY 305 SPFLYLQCLSQKLRQER 321

DB 241 SPFLYLQCLSQKLRQER 257

RESULT 4

AAV05790 standard; protein; 264 AA.

AC AAV05790;
 XX 02-AUG-1999 (first entry)
 DT
 XX Human anti-apoptotic MRIT-ND2 fragment.

XX MRIT-ND2, MACH related inducer of toxicity; human; apoptosis;

KM anti-apoptotic; cancer; autoimmune disease; angiogenesis;

KM atherosclerosis; neurodegenerative disease; Alzheimer's disease;

KM Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;

KM aplastic anaemia; myocardial infarction; therapy; mutant.

XX Homo sapiens.

OS Synthetic.

PN W09918230-A2.

PD 15-APR-1999.

PF 07-OCT-1998; 98MO-US021132.

PR 07-OCT-1997; 97US-00946226.

PA (UNIW) UNIV WASHINGTON.

PI Chaudhary PM;

DR WPI; 1999-277275/23.

PT Identifying regulators of MACH-related inducer of toxicity.

PS Claim 17; Page; 78pp; English.

XX The present sequence represents MRIT-ND2, comprising amino acid residues
 CC 217-480 of novel human MACH-related inducer of toxicity MRIT alpha 1 (see
 CC AAY05787). MRIT-ND2 has anti-apoptotic activity, as exemplified by the
 CC ability to suppress apoptosis mediated by a TNF family receptor in BHK or
 CC HeLa cells. The invention provides multiple isoforms of MRIT (see
 CC AAY05787-89), isolated active fragments of which have either pro-
 CC apoptotic or anti-apoptotic activity. Selective enhancers and inhibitors
 CC of MRIT apoptotic activity can be identified and used to treat diseases
 CC mediated by the dysfunction of programmed cell death or proliferation. A
 CC cell accumulation disorder such as cancer, autoimmune disease, viral
 CC infection, angiogenesis or atherosclerosis is treated by administering an
 CC agent that selectively enhances MRIT apoptotic activity, thereby inducing
 CC apoptosis in a subject. A disorder of cell loss, such as a
 CC neurodegenerative disorder, including Alzheimer's disease, Parkinson's
 CC disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial
 CC infarction or AIDS is treated by administering an agent that selectively
 CC inhibits MRIT apoptotic activity. Note: the present sequence is not shown
 CC in the specification but is derived from the MRIT alpha 1 sequence given
 CC in figure 1F

XX Sequence 264 AA;

Query Match 62.7%; Score 1128; DB 2; Length 264;
 Best Local Similarity 98.6%; Pred. No. 1.5e-104;
 Matches 213; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 106 REEPYKKSIOSEAFIPQSIPPEERYKMSKPLGICLIIDICIGNETELDRDFTSLGYEVQ 165

DB 4 QOEPYKKSIOSEAFIPQSIPPEERYKMSKPLGICLIIDICIGNETELDRDFTSLGYEVQ 63

QY 166 KFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGSSQSVYGVDTQHSGLPLHHRM 225

DB 64 KFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGSSQSVYGVDTQHSGLPLHHRM 123

QY 226 FMGDSQCYLLAGKPMFEITQNYVVSQGLDESSLLEVDPGPAKNVFEKAKRGKGLCTVHREA 285

DB 124 FMGDSQCYLLAGKPMFEITQNYVVSQGLDESSLLEVDPGPAKNVFEKAKRGKGLCTVHREA 183

QY 286 DFFWLSCTADMSLLEQSHSPFLYLQCLSQKLRQER 321

RESULT 7
AA05794
ID AA05794 standard; protein: 175 AA.
XX
AC AA05794;
XX
02-AUG-1999 (first entry)
XX
MRIT-D/S polypeptide.
XX
MRIT-D/S; MACH related inducer of toxicity; human; apoptosis;
XX anti-apoptotic; cancer; autoimmune disease; angiogenesis;
XX Alzheimer's disease; neurodegenerative disease; Alzheimer's disease;
XX Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
XX aplastic anaemia; myocardial infarction; therapy; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO9918230-A2.
XX
PD 15-APR-1999.
XX
PF 07-OCT-1998; 98MO-US021132.
XX
PR 07-OCT-1997; 97US-00946226.
XX
PA (UNIM) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
XX WPI; 1999-277275/23.
XX
PT Identifying regulators of MACH-related inducer of toxicity.
XX
PS Example 2; Page: 79pp; English.
XX
The present sequence represents MRIT-D/S, comprising amino acid residues 306-480 of novel human MACH-related inducer of toxicity MRIT alpha 1 (see AA057877). This deletion mutant was used to examine the interaction of MRIT alpha 1 with caspases. The FLICE-P20 domain interacted with MRIT alpha 1 but not with MRIT-D/S. The invention provides multiple isoforms of MRIT (see AA05787-89), isolated active fragments of which have either pro-apoptotic or anti-apoptotic activity. Selective enhancers and inhibitors of MRIT apoptotic activity can be identified and used to treat diseases mediated by the dysfunction of programmed cell death or proliferation, such as cancer or a neurodegenerative disorder. Note: the present sequence is not shown in the specification but is derived from the MRIT alpha 1 sequence given in figure 1F

XX
SQ Sequence 175 AA;
Query Match 37.9%; Score 683; DB 2; Length 175;
Best Local Similarity 99.2%; Pred. No. 4.6e-60;
Matches 129; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 192 DSFEVCVVSRSQSVYGVNDTSG;PLHRIHREMFMDGSCPYLAGKPKKFFIIONVVSQG 251
DB 1 DSFEVCVVSRSQSVYGVNDTSG;PLHRIHREMFMDGSCPYLAGKPKKFFIIONVVSQG 60
QY 252 QLEDDSSILEVDGPAKMKVEFKAKRG;CTVHREADFFWSLCTADMSLLEQSHSSPSLYLQ 311
DB 61 QLEDDSSILEVDGPAKMKVEFKAKRG;CTVHREADFFWSLCTADMSLLEQSHSSPSLYLQ 120
QY 312 CLSGKLRQER 321
DB 121 CLSGKLRQER 130

RESULT 8
AAE26110

AAE26110 standard; protein: 270 AA.
XX
AC AAE26110;
XX
DT 14-NOV-2002 (first entry)
XX
DE Human FLAME-1b protein.
XX
KW Human; FADD-like apoptotic/anti-apoptotic protein; Alzheimer's disease;
KW gene therapy; human immunodeficiency virus; HIV infection; apoptosis;
KW FLAME-1b.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 232..270
XX /note="FLAME-1b unique region"
XX
XX US2002086983-A1.
XX
XX 04-JUL-2002.
XX
XX 22-AUG-2001; 2001US-00935223.
XX
XX 28-OCT-1997; 97US-00959167.
XX
XX 26-MAR-1999; 99US-00276993.
XX
XX 28-NOV-2000; 2000US-00723450.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2002-642259/69.
XX
XX Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting
XX apoptosis, treating diseases characterized by apoptosis e.g. HIV
XX infection and Alzheimer's disease, and for identifying modulators of the
XX protein.
XX
XX Example; Fig 1a; 35pp; English.
XX
XX The invention relates to FADD-like apoptotic/anti-apoptotic proteins
XX (FLAME 1 or 2) and nucleic acid molecules encoding such proteins. FLAME
XX sequences are useful for inhibiting apoptosis and for gene therapy of
XX diseases characterised by apoptosis including HIV infection and
XX Alzheimer's disease. FLAME inhibitors are useful as apoptotic agents and
XX activators are useful as anti-apoptotic agents. FLAME-1 is useful as a
XX substrate for caspase in assays to identify caspase inhibitors. The
XX present sequence is human FLAME-1b protein

XX
SQ Sequence 270 AA;
Query Match 36.8%; Score 661.5; DB 5; Length 270;
Best Local Similarity 88.8%; Pred. No. 1.3e-57;
Matches 135; Conservative 0; Mismatches 0; Indels 17; Gaps 1;
QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGKRSKESFELDLVELEKLNIVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGKRSKESFELDLVELEKLNIVAPDQDLLEKCL 156
QY 61 KNTHRIDLKTIKYQSVQAGTSTRNVLQAAIQSLKDPENNFRREBPVKKSIOESNAF 120
DB 157 KNTHRIDLKTIKYQSVQAGTSTRNVLQAAIQSLKDPENNFRREBPVKKSIOESNAF 202
QY 121 LPQSIPEERYKMSKPLGCLIIIDCIGNETEL 152
DB 203 ---SIPBERYKMSKPLGCLIIIDCIGNETEL 231

RESULT 9
AA05795
ID AA05795 standard; protein: 227 AA.
XX

```

AC AAY05795;
XX
XX 02-AUG-1999 (first entry)
DT
XX
XX MRIT beta 2 polypeptide.
DE
XX
XX MRIT beta 2; MACH related inducer of toxicity; human; apoptosis;
XX anti-apoptotic; cancer; autoimmune disease; angiogenesis;
XX atherosclerosis; neurodegenerative disease; Alzheimer's disease;
XX Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
XX aplastic anaemia; myocardial infarction; therapy; mutant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO9918230-A2.
XX
XX 15-APR-1999.
XX
XX 07-OCT-1998; 98WO-US021132.
XX
XX 07-OCT-1997; 97US-00946226.
XX
XX (UNIM ) UNIV. WASHINGTON.
XX
XX Chaudhary FM;
XX
XX WPI; 1999-277275/23.
XX
XX Identifying regulators of MACH-related inducer of toxicity.
XX
XX Example 2; Page; 78pp; English.
XX
XX The present sequence represents MRIT beta 2, comprising amino acid
XX residues 1-227 of novel human MACH-related inducer of toxicity MRIT alpha
XX 1 (see AAY05787). This deletion mutant was used to examine the
XX interaction of MRIT alpha 1 with caspases. The results indicated that the
XX C-terminal 216 residues of MRIT are not sufficient for FLICE-P20
XX interaction. The invention provides multiple isoforms of MRIT (see
XX AAY05787-89), isolated active fragments of which have either pro-
XX apoptotic or anti-apoptotic activity. Selective enhancers and inhibitors
XX of MRIT apoptotic activity can be identified and used to treat diseases
XX mediated by the dysfunction of programmed cell death or proliferation,
XX such as cancer or a neurodegenerative disorder. Note: the present
XX sequence is not shown in the specification but is derived from the MRIT
XX alpha 1 sequence given in figure 1F
XX
XX Sequence 227 AA;
SQ
Query Match 30.0%; Score 540; DB 2; Length 227;
Best Local Similarity 85.5%; Pred. No. 1.6e-45;
Matches 112; Conservative 1; Mismatches 0; Indels 18; Gaps 1;
QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESKESFLDLVLEKLNVAPODLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESKESFLDLVLEKLNVAPODLDLEKCL 156
QY 61 KNHRIIDLKTKIQTKYKOSVQAGTSYRNVLQAAIQKSLKDPSSNFR----- 106
DB 157 KNHRIIDLKTKIQTKYKOSVQAGTSYRNVLQAAIQKSLKDPSSNFRILHNGRSKEQKLKQ 216
QY 107 ----EEPYKKS 113
DB 217 LGAQGEPPYKKS 227

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XX
XX Human G1 protein isoform beta (CASH-beta).
DE
XX
XX G1 protein; CASH-beta; human; caspase homologue; Fas receptor; modulator;
XX apoptosis; cell death; inflammation; tumour; HIV; therapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX Domain 2..73
XX /note="death domain/MORT module"
XX Domain 93..142
XX /note="death domain/MORT module"
XX
XX WO9839435-A1.
XX
XX 11-SEP-1998.
XX
XX 26-FEB-1998; 98WO-IL000098.
XX
XX 03-MAR-1997; 97IL-00120367.
XX 01-MAY-1997; 97IL-00120759.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Wallach D, Goltsev Y, Kovalenko A, Varfolomeev E, Brodianski V;
XX WPI; 1998-495842/42.
XX
XX N-PSDB; AAV52969.
XX
XX New DNA encoding isoforms of G1 protein which bind MORT-1 - and regulate
XX the effects of Fas and tumour necrosis factor receptors, useful for
XX killing of cells e.g. HIV and cancer cells.
XX
XX Claim 13; Fig 2; 13pp; English.
XX
XX This is the amino acid sequence of the beta isoform of novel human G1
XX protein. The sequence is deduced from an isolated skin fibroblast cDNA
XX clone (see AAV52969). G1-beta (also called CASH beta, CASH being caspase
XX homologue) and a longer isoform, G1-alpha (see AAV78903), represent 2
XX splice variants of the G1 protein. These G1 proteins are capable of
XX binding to, or interacting directly or indirectly, via their N-terminal
XX MORT modules, with MORT-1 or with MORT-binding proteins such as Mch4
XX (CASP-10) and MACH (CASP-8), and thereby of binding to the intracellular
XX domain of the Fas-R receptor, to which MORT-1 binds, or of binding to the
XX intracellular domain of the p55 tumour necrosis factor (TNF) receptor, to
XX which TRADD binds and to which TRADD protein MORT-1 binds. Hence, they
XX are considered as mediators or modulators of Fas-R having a role in e.g.
XX the signalling process that is initiated by the binding of Fas ligand to
XX Fas-R, and also having a role in the signalling process initiated by the
XX binding of TNF to p55-R. The longer isoform also has a C-terminal caspase
XX activity region involved in cytotoxic activity. G1 DNA (I) and
XX polypeptide (II), vectors and fragments are used to regulate cell death
XX or inflammatory processes. (II) is used to inhibit cell death, and its
XX inhibitors augment/enhance the processes. (I) and (II) regulate the Fas-R
XX ligand or TNF effect on cells carrying an Fas-R or p55-R. Tumour, HIV-
XX infected or other diseased cells can be treated using a viral vector
XX encoding a viral surface protein, which binds a specific cell surface
XX receptor and a sequence encoding (II), which kills the cell. Antisense
XX oligonucleotides, introduced using the above vector, block the expression
XX of (II) and can also regulate the above effects. These effects can also
XX be regulated using a vector encoding a ribozyme that interacts with a
XX cellular mRNA encoding (II), and allows (II) expression
XX
XX Sequence 221 AA;
SQ
Query Match 29.3%; Score 527; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.2e-44;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESKESFLDLVLEKLNVAPODLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESKESFLDLVLEKLNVAPODLDLEKCL 156

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QY 61 KNHRIDLTKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPSPNNR 106
 DB 157 KNHRIDLTKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPSPNNR 202

RESULT 11
 ID AAM76630 standard; protein; 221 AA.

AC AAM76630;
 DT 12-JUL-1999 (first entry)

DE Human CFLIP-S protein.

KM Death effector domain; human; murine; anti-apoptotic; treatment;
 KW HIV infection; autoimmune disease; FLIP protein.

OS Homo sapiens.

PN DE19713393-A1.

PD 08-OCT-1998.

PF 01-APR-1997; 97DE-01013393.

PR 01-APR-1997; 97DE-01013393.

XX (TSCH/) TSCHOPP J.

XX Tschoopp J, Thome M, Burns K, Irmeler M, Hahne M, Schroeter M;
 PI Schneider P, Bodmer J, Steiner V, Rimoldi D, Hoffmann K, French EL;
 DR WPI: 1998-532710/46.

XX N-PSDB; AAV61936.

XX

PT New DNA encoding for anti-apoptotic gene product - used to treat HIV
 PT infections and autoimmune diseases.

PS Claim 20; Fig 4A; 45pp; German.

CC This invention describes novel human and mouse anti-apoptotic gene
 CC products which contain at least one death effector domain. The products
 CC of the invention are used in the treatment of HIV infections and
 CC autoimmune diseases

XX Sequence 221 AA;

Query Match 29.3%; Score 527; DB 2; Length 221;
 Best Local Similarity 100.0%; Pred. No. 3.2e-44;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVLEKINLVAPDQDLLEKCL 60
 DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVLEKINLVAPDQDLLEKCL 156
 QY 61 KNHRIDLTKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPSPNNR 106
 DB 157 KNHRIDLTKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPSPNNR 202

RESULT 12
 ID AAY05789 standard; protein; 221 AA.

AC AAY05789;

DT 02-AUG-1999 (first entry)

XX Human MACH related inducer of toxicity WRIT beta 1.

XX WRIT beta 1; MACH related inducer of toxicity; human; apoptosis;

KW pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
 KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
 KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
 KW aplastic anaemia; myocardial infarction; therapy.

OS Homo sapiens.

PN W09918230-A2.

PD 15-APR-1999.

PF 07-OCT-1998; 98WO-US021132.

PR 07-OCT-1997; 97US-00946226.

XX (UNIV) UNIV WASHINGTON.

PI Chaudhary PM;

DR WPI: 1999-277275/23.

DR N-PSDB; AAX25510.

PT Identifying regulators of MACH-related inducer of toxicity.

PS Example 1; Fig 1H; 78pp; English.

CC The present sequence represents novel human MACH-related inducer of
 CC toxicity (WRIT) isoform WRIT beta 1, a CED-4 homologue. Multiple isoforms
 CC of WRIT have been identified, some of which function to induce caspase
 CC dependent apoptosis in mammalian cells, e.g. WRIT alpha 1 (see AAY05787)
 CC and WRIT beta 1, while others have anti-apoptotic activity, e.g. WRIT
 CC alpha 2 (see AAY05788). WRIT beta 1 lacks the N-terminal death effector
 CC domain of WRIT alpha 1 but includes a C-terminal caspase ICE homology
 CC domain region. Selective enhancers and inhibitors of WRIT apoptotic
 CC activity can be identified and used to treat diseases mediated by the
 CC dysfunction of programmed cell death or proliferation. A cell
 CC accumulation disorder such as cancer, autoimmune disease, viral
 CC infection, angiogenesis or atherosclerosis is treated by administering an
 CC agent that selectively enhances WRIT apoptotic activity, thereby inducing
 CC apoptosis in a subject. A disorder of cell loss, such as a
 CC neurodegenerative disorder, including Alzheimer's disease, Parkinson's
 CC disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial
 CC infarction or AIDS can be treated by administering an agent that
 CC selectively inhibits WRIT apoptotic activity

XX Sequence 221 AA;

Query Match 29.3%; Score 527; DB 2; Length 221;
 Best Local Similarity 100.0%; Pred. No. 3.2e-44;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVLEKINLVAPDQDLLEKCL 60
 DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVLEKINLVAPDQDLLEKCL 156
 QY 61 KNHRIDLTKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPSPNNR 106
 DB 157 KNHRIDLTKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPSPNNR 202

RESULT 13
 ID AAY57455 standard; protein; 221 AA.

AC AAY57455;

DT 25-FEB-2000 (first entry)

XX Human FLICE-like inhibitory protein short form protein sequence.

XX Human, FLICE-like inhibitory protein long form; FLIP-L; FLIP-S;
 KW FLICE-like inhibitory protein short form; apoptosis inhibitor;
 KW atherosclerosis; vascular wall inflammation; vascular injury;

XX Hood L, Chaudhary PM;
PI
XX
DR WPI; 2001-101569/11.
XX
PT Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
PT for therapeutic purposes.
XX
PS Example 8; Col 43-46; 60pp; English.
XX
CC The present sequence has been shown to regulate the nuclear factor-kappa
CC B (NF-kB), Jun N-terminal kinase (JNK) and apoptosis pathways. It is
CC provided in a specification relating to novel mutants (D73A, L74A and
CC L75A) for Caspase-8, which are also useful for regulating NF-kB, JNK and
CC apoptosis activities. The Caspase-8 mutants are useful for therapeutic
CC purposes and in test methods or assays for determining whether a
CC candidate compound has a significant effect upon cell activities,
CC especially NF-kB, JNK and apoptosis, so as to facilitate the discovery
CC and/or design of therapeutic agents
XX
SQ Sequence 221 AA;

Query March 29.3%; Score 527; DB 4; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.2e-44;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEIGEDLDKSDVSSLIFFLMKDYMGKISKEKSFLLDLYVELEKLNVAPOQLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIFFLMKDYMGKISKEKSFLLDLYVELEKLNVAPOQLLEKCL 156
QY 61 KNHRIIDLKTKIQKYSVQAGTSYRNVLQAAIQKSLKDPNNFR 106
DB 157 KNHRIIDLKTKIQKYSVQAGTSYRNVLQAAIQKSLKDPNNFR 202

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OM protein - protein search, using sw model

Run on: September 8, 2004, 06:26:47 ; Search time 127 Seconds

(without alignments)
863.328 Million cell updates/sec

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Perfect score: 1800
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Searched: 1298764 segs, 315065143 residues

Total number of hits satisfying chosen parameters: 980710

Minimum DB seq length: 0
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Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 1800 | 100.0 | 348 | US-09-009-893-6 | Sequence 6, Appl1 |
| 2 | 1800 | 100.0 | 348 | US-10-713-208-6 | Sequence 6, Appl1 |
| 3 | 527 | 29.3 | 221 | US-09-410-194-15 | Sequence 15, Appl1 |
| 4 | 527 | 29.3 | 221 | US-09-410-194-22 | Sequence 22, Appl1 |
| 5 | 391 | 21.7 | 76 | US-09-864-761-35073 | Sequence 35073, A |
| 6 | 277 | 15.4 | 56 | US-10-627-571-5 | Sequence 5, Appl1 |
| 7 | 277 | 15.4 | 56 | US-10-627-571-7 | Sequence 7, Appl1 |
| 8 | 261.5 | 14.5 | 335 | US-10-368-438-16 | Sequence 16, Appl1 |
| 9 | 237 | 13.2 | 56 | US-10-627-571-6 | Sequence 16, Appl1 |
| 10 | 228 | 12.7 | 286 | US-09-862-915-1 | Sequence 1, Appl1 |
| 11 | 225.5 | 12.5 | 59 | US-10-627-571-4 | Sequence 4, Appl1 |
| 12 | 215 | 11.9 | 266 | US-10-368-438-20 | Sequence 20, Appl1 |
| 13 | 199 | 11.1 | 293 | US-09-954-697-21 | Sequence 21, Appl1 |
| 14 | 199 | 11.1 | 293 | US-09-851-873-99 | Sequence 99, Appl1 |
| 15 | 199 | 11.1 | 293 | US-10-171-077-5 | Sequence 5, Appl1 |

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|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
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| US-10-280-670-6 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 |
| US-10-368-438-31 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | |
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| US-09-895-263-4 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | |
| US-10-232-884-4 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | |
| US-10-214-932-108 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | |
| US-10-207-655-202 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | |
| US-10-954-697-34 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | 290 | |
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| US-09-851-873-98 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | |
| US-10-280-670-5 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | |
| US-10-368-438-30 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | |
| US-10-408-765A-172 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | |
| US-10-701-490-11 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | 277 | |
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| US-09-954-697-24 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | |
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| US-09-851-873-100 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | |
| US-10-337-060-2 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | |
| US-10-280-670-4 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | |
| US-10-214-932-110 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | |

ALIGNMENTS

RESULT 1
US-09-009-893-6
Sequence 6, Application US/09009893
Publicat ion No. US20030087339A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: 1-FLICE, A NOVEL INHIBITOR OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,893
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-009-893-6

Query Match 100.0%; Score 1800; DB 10; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.1e-170;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVVELEKLNVAAPDQDLLEKCL 60
DB 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVVELEKLNVAAPDQDLLEKCL 60
QY 61 KNHRIIDLTKTKIQKYKQSVQAGTSYRNVLOAAIQKSLKDPNNFREPVKKSIOSEAF 120
DB 61 KNHRIIDLTKTKIQKYKQSVQAGTSYRNVLOAAIQKSLKDPNNFREPVKKSIOSEAF 120
QY 121 LPOSIPERIRYKMSKPLIGLIIIDCIGNETELRDFTSLGYEVQKFLHSMHGISOILG 180
DB 121 LPOSIPERIRYKMSKPLIGLIIIDCIGNETELRDFTSLGYEVQKFLHSMHGISOILG 180
QY 181 QFACMPERHDYDSFVCYLVSRGSGQSVYGVDTSGPLPHIRRMFGDSCPYLAGKPRM 240
DB 181 QFACMPERHDYDSFVCYLVSRGSGQSVYGVDTSGPLPHIRRMFGDSCPYLAGKPRM 240
QY 241 FFIQNYVVSQGLESDSLLEVDPGPKMNVFPAQKRGCLCTVHREADFFWMSLCTADMSLE 300
DB 241 FFIQNYVVSQGLESDSLLEVDPGPKMNVFPAQKRGCLCTVHREADFFWMSLCTADMSLE 300
QY 301 QSHSSPSLYLQCLSQKLRQERGTTPSGGTTESKDMHFSLSGCLLDVL 348
DB 301 QSHSSPSLYLQCLSQKLRQERGTTPSGGTTESKDMHFSLSGCLLDVL 348

RESULT 2

US-10-713-208-6
Sequence 6, Application US/10713208
Publication No. US20040121387A1
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: I-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 and
FILE REFERENCE: PF381C1D1
CURRENT APPLICATION NUMBER: US/10/713,208
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US 09/489,155
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/009,893
PRIOR FILING DATE: 1998-01-21
PRIOR APPLICATION NUMBER: US 60/054,800
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/034,205
PRIOR FILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapiens
US-10-713-208-6

Query Match 100.0%; Score 1800; DB 16; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.1e-170;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVVELEKLNVAAPDQDLLEKCL 60

DB 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVVELEKLNVAAPDQDLLEKCL 60
QY 61 KNHRIIDLTKTKIQKYKQSVQAGTSYRNVLOAAIQKSLKDPNNFREPVKKSIOSEAF 120
DB 61 KNHRIIDLTKTKIQKYKQSVQAGTSYRNVLOAAIQKSLKDPNNFREPVKKSIOSEAF 120
QY 121 LPOSIPERIRYKMSKPLIGLIIIDCIGNETELRDFTSLGYEVQKFLHSMHGISOILG 180
DB 121 LPOSIPERIRYKMSKPLIGLIIIDCIGNETELRDFTSLGYEVQKFLHSMHGISOILG 180
QY 181 QFACMPERHDYDSFVCYLVSRGSGQSVYGVDTSGPLPHIRRMFGDSCPYLAGKPRM 240
DB 181 QFACMPERHDYDSFVCYLVSRGSGQSVYGVDTSGPLPHIRRMFGDSCPYLAGKPRM 240
QY 241 FFIQNYVVSQGLESDSLLEVDPGPKMNVFPAQKRGCLCTVHREADFFWMSLCTADMSLE 300
DB 241 FFIQNYVVSQGLESDSLLEVDPGPKMNVFPAQKRGCLCTVHREADFFWMSLCTADMSLE 300
QY 301 QSHSSPSLYLQCLSQKLRQERGTTPSGGTTESKDMHFSLSGCLLDVL 348
DB 301 QSHSSPSLYLQCLSQKLRQERGTTPSGGTTESKDMHFSLSGCLLDVL 348

RESULT 3

US-09-410-194-15
Sequence 15, Application US/09410194
Patent No. US20020095030A1
GENERAL INFORMATION:
APPLICANT: Tschopp, Jurg
APPLICANT: Thome, Margot
APPLICANT: Burns, Kimberly
APPLICANT: Imbler, Marten
APPLICANT: Hahne, Michael
APPLICANT: Schroeder, Michael
APPLICANT: Schneider, Pascal
APPLICANT: Bodmer, Jean-Luc
APPLICANT: Steiner, Veronique
APPLICANT: Rimoldi, Donata
APPLICANT: Hoffmann, Kay
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 1141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
US-09-410-194-15

Query Match 29.3%; Score 527; DB 9; Length 221;
Best Local Similarity 100.0%; Pred. No. 8.3e-44;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVVELEKLNVAAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVVELEKLNVAAPDQDLLEKCL 156
QY 61 KNHRIIDLTKTKIQKYKQSVQAGTSYRNVLOAAIQKSLKDPNNFREPVKKSIOSEAF 106
DB 61 KNHRIIDLTKTKIQKYKQSVQAGTSYRNVLOAAIQKSLKDPNNFREPVKKSIOSEAF 106

RESULT 4
US-09-410-194-22
Sequence 22, Application US/09410194

```
Patent No. US20020095030A1
GENERAL INFORMATION:
APPLICANT: Teschopp, Jung
APPLICANT: Thome, Margot
APPLICANT: Burns, Kimberly
APPLICANT: Imbler, Marten
APPLICANT: Hahne, Michael
APPLICANT: Schroter, Michael
APPLICANT: Schneider, Pascal
APPLICANT: Bodmer, Jean-Luc
APPLICANT: Steiner, Veronique
APPLICANT: Rimoldi, Donata
APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
US-09-410-194-22

Query Match      29.3%; Score 527; DB 9; Length 221;
Best Local Similarity 100.0%; Pred. No. 8.3e-44;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  MAEIGELDSDVSLIFLMDYMGKISKESFIDLVELEKLNIVAPDLDLEKCL 60
Db      97  MAEIGELDSDVSLIFLMDYMGKISKESFIDLVELEKLNIVAPDLDLEKCL 156

Oy      61  KNIRIDLTIKIKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR 106
Db      157 KNIRIDLTIKIKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR 202

RESULT 5
US-09-864-761-35073
Sequence 35073, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/633,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263, 6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35073
LENGTH: 76
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007283.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.9
OTHER INFORMATION: EST_HUMAN HIT: A1139524.1, EVALUE 2.00e-38
US-09-864-761-35073

Query Match      21.7%; Score 391; DB 9; Length 76;
Best Local Similarity 98.7%; Pred. No. 5.7e-31;
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      245  NYVVSQGLDSSLLVDDPAMKNVEFKQKRGCTVHREADFMSICTADMSLEQSHS 304
Db      1  NYVVSQGLDSSLLVDDPAMKNVEFKQKRGCTVHREADFMSICTADMSLEQSHS 60

Oy      305  SPSLYICLSQKLRQE 320
Db      61  SPSLYICLSQKLRQE 76

RESULT 6
US-10-627-571-5
Sequence 5, Application US/10627571
Publication No. US20040082771A1
GENERAL INFORMATION:
APPLICANT: KASID, Usha N.
APPLICANT: KUMAR, Deepak
APPLICANT: GOKHALE, Pritulula
APPLICANT: AHYAD, Imran
TITLE OF INVENTION: ANTI-APOTOTIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USES
FILE REFERENCE: 223316
CURRENT APPLICATION NUMBER: US/10/627,571
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 60/264,062
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/US02/02212
PRIOR FILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 25
```

SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: CASH Alpha/Beta - fragment
US-10-627-571-5

Query Match 15.4%; Score 277; DB 16; Length 56;
Best Local Similarity 100.0%; Pred. No. 8e-20;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SDVSSLIPLMKDYMGRGKISKEKSFLLVLELEKLNIVAPDQDLLEKCKLNHRI 66
DB 1 SDVSSLIPLMKDYMGRGKISKEKSFLLVLELEKLNIVAPDQDLLEKCKLNHRI 56

RESULT 7
US-10-627-571-7
Sequence 7, Application US/10627571
Publication No. US20040082771A1
GENERAL INFORMATION:
APPLICANT: KASID, Usha N.
APPLICANT: KUMAR, Deepak
APPLICANT: GOKHALE, Prafulla
APPLICANT: AHMAD, Imran
TITLE OF INVENTION: ANTI-APOTOPIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USES
FILE REFERENCE: 22316
CURRENT APPLICATION NUMBER: US/10/627,571
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 60/264,062
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/US02/02212
PRIOR FILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: MISC FEATURE
NAME/KEY: MISC FEATURE
OTHER INFORMATION: FLIP (L) - fragment
US-10-627-571-7

Query Match 15.4%; Score 277; DB 16; Length 56;
Best Local Similarity 100.0%; Pred. No. 8e-20;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SDVSSLIPLMKDYMGRGKISKEKSFLLVLELEKLNIVAPDQDLLEKCKLNHRI 66
DB 1 SDVSSLIPLMKDYMGRGKISKEKSFLLVLELEKLNIVAPDQDLLEKCKLNHRI 56

RESULT 8
US-10-368-438-16
Sequence 16, Application US/10368438
Publication No. US20030219411A1
GENERAL INFORMATION:
APPLICANT: David WALLACH
Mark P. BOLDIN
Tanya M. GONCHAROV
Tanya V. GOLTSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESS: Broadway and Newmark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/368,438
FILING DATE: 20-Feb-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Broadway, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-368-438-16

Query Match 14.5%; Score 261.5; DB 15; Length 335;
Best Local Similarity 26.6%; Pred. No. 4.2e-17;
Matches 86; Conservative 60; Mismatches 108; Indels 69; Gaps 13;

QY 28 KISKESFLVLELEKLNIVAPDQDLLEKCKLNHRIIDLTXTQYKQSGVQSGSYR 87
DB 3 KLDDDMNLDTFLEMERYVILGKIDILKVCQAQINKSLKI-INDYBSRSKSELG-- 59
QY 88 NVLAALQKSLKDPNSNFFREBPYKSIQSEAFLLPQSIPEERYKXKXPLGICLIIDIG 147
DB 60 -----GWMITISDPRE-----QSES---QTL-DKYQKSKRPGYCLIIHNH 99
QY 148 -----NETEL-----LNDTFSIGYEVKFLHLSMNGISQILGFPACMP 186
DB 100 FAYAREKVPKLSIRDRNGTHLDAGALTTTFELHFEIRPHDDCTVEBOIYEIWKIYQLM- 158
QY 187 EHRDYDFVCVLVSRGSGSVYGVDTGSLPLHIRMFMGDSCTYLAGKXMPFIQ-- 244
DB 159 DHNMOCFICILSHDKGIITGDSQEG--PIYELTSGFTGLKCPSLAGKXKVFETAC 216
QY 245 ---NY---VYSQQLDSSSLEVD--GPMKQVVERKQKRGICLYHRADPFWMSCTADM 296
DB 217 QGDNYYKGIPIVEDSEOPYLEMDLSSPOTRYIP-----DEADFLGATVNN 264
QY 297 SLLEQSHSPSYLQCTSQKRO 319
DB 265 CVGYRNPABEGTWIQTSLQSLRE 287

RESULT 9

RESULT 15

US-10-171-077-5

Sequence 5; Application US/10171077

Publication No. US20030022353A1

GENERAL INFORMATION:

APPLICANT: Litwack, Gerald

Alnemri, Emdad S.

Fernandez-Alnemri, Teresa

PROTEASE

TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE

AND COMPOSITIONS FOR MAKING AND

METHODS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSSEE: Woodcock, Washburn, Kurtz, Mackiewicz &

No. US20030022353A1 is

STREET: One Liberty Place, 46th floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/171,077

FILING DATE: 12-Jun-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/446,925

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TUU-1508

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 293 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-171-077-5

Query Match 11.1%; Score 199; DB 14; Length 293;

Best Local Similarity 27.5%; Pred. No. 5, 7e-11;

Matches 69; Conservative 33; Mismatches 75; Indels 74; Gaps 10;

111 KKSIOSEAPLPQSI--PEERYKXKSKPLGICLIID-----CIGNETEL 152

16 EENMETETDAFYKREMPDPAEKYKMDHRRGIALIFNHERPFMTLPERRRTCADRDN-- 73

153 LADFTSLGYEVQKE-----LHLSMHGTSQILGQFACMPEHRDYSFYCVLVSRGSSQ 205

74 LTRRRPSDLGFVVKCFNDIKAEELLLKIHEVSTV-----SHADADCFYCVFLSHGEGN 125

206 SVYGYD-----QTSGLPLHHRIRMFMDSCPYLAGKPKMFFIQ-----NYVY 248

126 HIYAVDAKIEIQTLTGL-----FKGDKCHSLVAKPKIFIIQACRGQHDVPIPLDV 177

249 SDGQLE--DSSLLEVDPAMKGVFFKQKRGKGLCTVHRADPFWSLCTADKSLLEQSHSSP 306

178 VDNQTEKLDITNITEVDAAS-----VYTLPAQADFLMCYSVAEGYYSRHRTVNG 225

307 SYVLOCTSQKL 317

226 SWYIDLCLEML 236

Search completed: September 8, 2004, 06:37:53
Job time : 128 secs

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